PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : C12N 15/31, C07K 14/315, 16/12, C12Q 1/68

A2

(11) International Publication Number: WO 98/18931

(43) International Publication Date: 7 May 1998 (07.05.98)

(21) International Application Number: PCT/US97/19588

(22) International Filing Date: 30 October 1997 (30.10.97)

(30) Priority Data:
60/029,960 31 October 1996 (31.10.96) US

(71) Applicant *(for all designated States except US)*: HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).

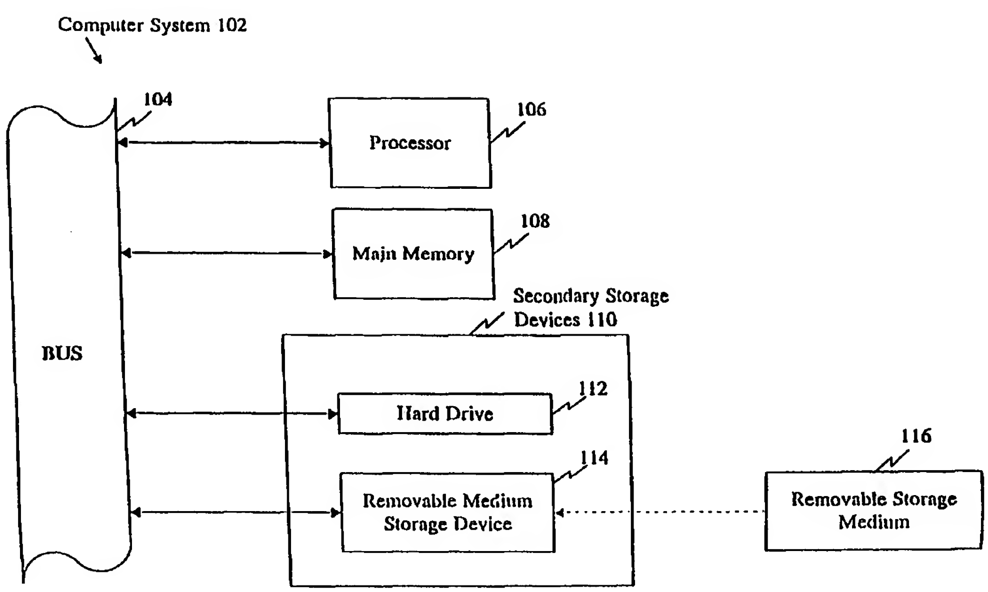
(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: KUNSCH, Charles, A. [US/US]; 2398B Dunwoody Crossing, Atlanta, GA 30338 (US). CHOI, Gil, H. [KR/US]; 11429 Potomac Oaks Drive, Rockville, MD 20850 (US). DILLON, Patrick, J. [US/US]; 1055 Snipe Court, Carlsbad, CA 92009 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hill Road, Laytonsville, MD 20882 (US). BARASH, Steven, C. [US/US]; 582 College Parkway #303, Rockville, MD 20850 (US). FANNON, Michael [US/US]; 13501 Rippling Brook Drive, Silver Spring, MD 20850 (US). DOUGHERTY, Brian, A. [US/US]; 708 Meadow Field Court, Mount Airy, MD 21771 (US).

(74) Agents: BROOKES, A., Anders et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).

Published
Without international search report and to be republished upon receipt of that report.

(54) Title: *STREPTOCOCCUS PNEUMONIAE* POLYNUCLEOTIDES AND SEQUENCES



(57) Abstract

The present invention provides polynucleotide sequences of the genome of *Streptococcus pneumoniae*, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania
AM	Armenia
AT	Austria
AU	Australia
AZ	Azerbaijan
BA	Bosnia and Herzegovina
BB	Barbados
BE	Belgium
BF	Burkina Faso
BG	Bulgaria
BJ	Benin
BR	Brazil
BY	Belarus
CA	Canada
CF	Central African Republic
CG	Congo
CH	Switzerland
CI	Côte d'Ivoire
CM	Cameroon
CN	China
CU	Cuba
CZ	Czech Republic
DE	Germany
DK	Denmark
EE	Estonia
ES	Spain
FI	Finland
FR	France
GA	Gabon
GB	United Kingdom
GE	Georgia
GH	Ghana
GN	Guinea
GR	Greece
HU	Hungary
IE	Ireland
IL	Israel
IS	Iceland
IT	Italy
JP	Japan
KE	Kenya
KG	Kyrgyzstan
KP	Democratic People's Republic of Korea
KR	Republic of Korea
KZ	Kazakstan
LC	Saint Lucia
LI	Liechtenstein
LK	Sri Lanka
LR	Liberia
LS	Lesotho
LT	Lithuania
LU	Luxembourg
LV	Latvia
MC	Monaco
MD	Republic of Moldova
MG	Madagascar
MK	The former Yugoslav Republic of Macedonia
ML	Mali
MN	Mongolia
MR	Mauritania
MW	Malawi
MX	Mexico
NE	Niger
NL	Netherlands
NO	Norway
NZ	New Zealand
PL	Poland
PT	Portugal
RO	Romania
RU	Russian Federation
SD	Sudan
SE	Sweden
SG	Singapore
SI	Slovenia
SK	Slovakia
SN	Senegal
SZ	Swaziland
TD	Chad
TG	Togo
TJ	Tajikistan
TM	Turkmenistan
TR	Turkey
TT	Trinidad and Tobago
UA	Ukraine
UG	Uganda
US	United States of America
UZ	Uzbekistan
VN	Viet Nam
YU	Yugoslavia
ZW	Zimbabwe

Streptococcus pneumoniae Polynucleotides and Sequences

FIELD OF THE INVENTION

The present invention relates to the field of molecular biology. In particular, it relates to, among other things, nucleotide sequences of *Streptococcus pneumoniae*, contigs, ORFs, fragments, probes, primers and related polynucleotides thereof, peptides and polypeptides encoded by the sequences, and uses of the polynucleotides and sequences thereof, such as in fermentation, polypeptide production, assays and pharmaceutical development, among others.

BACKGROUND OF THE INVENTION

Streptococcus pneumoniae has been one of the most extensively studied microorganisms since its first isolation in 1881. It was the object of many investigations that led to important scientific discoveries. In 1928, Griffith observed that when heat-killed encapsulated pneumococci and live strains constitutively lacking any capsule were concomitantly injected into mice, the nonencapsulated could be converted into encapsulated pneumococci with the same capsular type as the heat-killed strain. Years later, the nature of this "transforming principle," or carrier of genetic information, was shown to be DNA. (Avery, O.T., *et al., J. Exp. Med., 79:*137-157 (1944)).

In spite of the vast number of publications on *S. pneumoniae* many questions about its virulence are still unanswered, and this pathogen remains a major causative agent of serious human disease, especially community-acquired pneumonia. (Johnston, R.B., *et al., Rev. Infect. Dis. 13*(Suppl. 6):S509-517 (1991)). In addition, in developing countries, the pneumococcus is responsible for the death of a large number of children under the age of 5 years from pneumococcal pneumonia. The incidence of pneumococcal disease is highest in infants under 2 years of age and in people over 60 years of age. Pneumococci are the second most frequent cause (after *Haemophilus influenzae* type b) of bacterial meningitis and otitis media in children. With the recent introduction of conjugate vaccines for *H. influenzae* type b, pneumococcal meningitis is likely to become increasingly prominent. *S. pneumoniae* is the most important etiologic agent of community-

acquired pneumonia in adults and is the second most common cause of bacterial meningitis behind *Neisseria meningitidis.*

The antibiotic generally prescribed to treat *S. pneumoniae* is benzylpenicillin, although resistance to this and to other antibiotics is found occasionally. Pneumococcal resistance to penicillin results from mutations in its penicillin-binding proteins. In uncomplicated pneumococcal pneumonia caused by a sensitive strain, treatment with penicillin is usually successful unless started too late. Erythromycin or clindamycin can be used to treat pneumonia in patients hypersensitive to penicillin, but resistant strains to these drugs exist. Broad spectrum antibiotics (e.g., the tetracyclines) may also be effective, although tetracycline-resistant strains are not rare. In spite of the availability of antibiotics, the mortality of pneumococcal bacteremia in the last four decades has remained stable between 25 and 29%. (Gillespie, S.H., *et al.*, *J. Med. Microbiol. 28:*237-248 (1989).

S. pneumoniae is carried in the upper respiratory tract by many healthy individuals. It has been suggested that attachment of pneumococci is mediated by a disaccharide receptor on fibronectin, present on human pharyngeal epithelial cells. (Anderson, B.J., *et al.*, *J. Immunol. 142*:2464-2468 (1989). The mechanisms by which pneumococci translocate from the nasopharynx to the lung, thereby causing pneumonia, or migrate to the blood, giving rise to bacteremia or septicemia, are poorly understood. (Johnston, R.B., *et al.*, *Rev. Infect. Dis. 13*(Suppl. 6):S509-517 (1991).

Various proteins have been suggested to be involved in the pathogenicity of *S. pneumoniae*, however, only a few of them have actually been confirmed as virulence factors. Pneumococci produce an IgA1 protease that might interfere with host defense at mucosal surfaces. (Kornfield, S.J., *et al.*, *Rev. Inf. Dis. 3*:521-534 (1981). *S. pneumoniae* also produces neuraminidase, an enzyme that may facilitate attachment to epithelial cells by cleaving sialic acid from the host glycolipids and gangliosides. Partially purified neuraminidase was observed to induce meningitis-like symptoms in mice; however, the reliability of this finding has been questioned because the neuraminidase preparations used were probably contaminated with cell wall products. Other pneumococcal proteins besides neuraminidase are involved in the adhesion of pneumococci to epithelial and endothelial cells. These pneumococcal proteins have as yet not been identified. Recently, Cundell *et. al.*, reported that peptide permeases can modulate

pneumococcal adherence to epithelial and endothelial cells. It was, however, unclear whether these permeases function directly as adhesions or whether they enhance adherence by modulating the expression of pneumococcal adhesions. (DeVelasco, E.A., *et al.*, *Micro. Rev.* *59*:591-603 (1995). A better understanding of the virulence factors determining its pathogenicity will need to be developed to cope with the devastating effects of pneumococcal disease in humans.

Ironically, despite the prominent role of *S. pneumoniae* in the discovery of DNA, little is known about the molecular genetics of the organism. The *S. pneumoniae* genome consists of one circular, covalently closed, double-stranded DNA and a collection of so-called variable accessory elements, such as prophages, plasmids, transposons and the like. Most physical characteristics and almost all of the genes of *S. pneumoniae* are unknown. Among the few that have been identified, most have not been physically mapped or characterized in detail. Only a few genes of this organism have been sequenced. (See, for instance current versions of GENBANK and other nucleic acid databases, and references that relate to the genome of *S. pneumoniae* such as those set out elsewhere herein.)

It is clear that the etiology of diseases mediated or exacerbated by *S. pneumoniae,* infection involves the programmed expression of *S. pneumoniae* genes, and that characterizing the genes and their patterns of expression would add dramatically to our understanding of the organism and its host interactions. Knowledge of *S. pneumoniae* genes and genomic organization would improve our understanding of disease etiology and lead to improved and new ways of preventing, ameliorating, arresting and reversing diseases. Moreover, characterized genes and genomic fragments of *S. pneumoniae* would provide reagents for, among other things, detecting, characterizing and controlling *S. pneumoniae* infections. There is a need to characterize the genome of *S. pneumoniae* and for polynucleotides of this organism.

SUMMARY OF THE INVENTION

The present invention is based on the sequencing of fragments of the *Streptococcus pneumoniae* genome. The primary nucleotide sequences which were generated are provided in SEQ ID NOS:1-391.

The present invention provides the nucleotide sequence of several hundred contigs of the *Streptococcus pneumoniae* genome, which are listed in tables below and set out in the Sequence Listing submitted herewith, and representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan. In one embodiment, the present invention is provided as contiguous strings of primary sequence information corresponding to the nucleotide sequences depicted in SEQ ID NOS:1-391.

The present invention further provides nucleotide sequences which are at least 95% identical to the nucleotide sequences of SEQ ID NOS:1-391.

The nucleotide sequence of SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-391 may be provided in a variety of mediums to facilitate its use. In one application of this embodiment, the sequences of the present invention are recorded on computer readable media. Such media includes, but is not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

The present invention further provides systems, particularly computer-based systems which contain the sequence information herein described stored in a data storage means. Such systems are designed to identify commercially important fragments of the *Streptococcus pneumoniae* genome.

Another embodiment of the present invention is directed to fragments of the *Streptococcus pneumoniae* genome having particular structural or functional attributes. Such fragments of the *Streptococcus pneumoniae* genome of the present invention include, but are not limited to, fragments which encode peptides, hereinafter referred to as open reading frames or ORFs, fragments which modulate the expression of an operably linked ORF, hereinafter referred to as expression modulating fragments or EMFs, and fragments which can be used to diagnose the

presence of *Streptococcus pneumoniae* in a sample, hereinafter referred to as diagnostic fragments or DFs.

Each of the ORFs in fragments of the *Streptococcus pneumoniae* genome disclosed in Tables 1-3, and the EMFs found 5' to the ORFs, can be used in numerous ways as polynucleotide reagents. For instance, the sequences can be used as diagnostic probes or amplification primers for detecting or determining the presence of a specific microbe in a sample, to selectively control gene expression in a host and in the production of polypeptides, such as polypeptides encoded by ORFs of the present invention, particular those polypeptides that have a pharmacological activity.

The present invention further includes recombinant constructs comprising one or more fragments of the *Streptococcus pneumoniae* genome of the present invention. The recombinant constructs of the present invention comprise vectors, such as a plasmid or viral vector, into which a fragment of the *Streptococcus pneumoniae* has been inserted.

The present invention further provides host cells containing any of the isolated fragments of the *Streptococcus pneumoniae* genome of the present invention. The host cells can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic cell, such as a yeast cell, or a procaryotic cell such as a bacterial cell.

The present invention is further directed to isolated polypeptides and proteins encoded by ORFs of the present invention. A variety of methods, well known to those of skill in the art, routinely may be utilized to obtain any of the polypeptides and proteins of the present invention. For instance, polypeptides and proteins of the present invention having relatively short, simple amino acid sequences readily can be synthesized using commercially available automated peptide synthesizers. Polypeptides and proteins of the present invention also may be purified from bacterial cells which naturally produce the protein. Yet another alternative is to purify polypeptide and proteins of the present invention from cells which have been altered to express them.

The invention further provides methods of obtaining homologs of the fragments of the *Streptococcus pneumoniae* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. Specifically, by using the nucleotide and amino acid sequences disclosed herein as

a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

The invention further provides antibodies which selectively bind polypeptides and proteins of the present invention. Such antibodies include both monoclonal and polyclonal antibodies.

The invention further provides hybridomas which produce the above-described antibodies. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

The present invention further provides methods of identifying test samples derived from cells which express one of the ORFs of the present invention, or a homolog thereof. Such methods comprise incubating a test sample with one or more of the antibodies of the present invention, or one or more of the DFs of the present invention, under conditions which allow a skilled artisan to determine if the sample contains the ORF or product produced therefrom.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the above-described assays.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the antibodies, or one of the DFs of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of bound antibodies or hybridized DFs.

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents capable of binding to a polypeptide or protein encoded by one of the ORFs of the present invention. Specifically, such agents include, as further described below, antibodies, peptides, carbohydrates, pharmaceutical agents and the like. Such methods comprise steps of: (a) contacting an agent with an isolated protein encoded by one of the ORFs of the present invention; and (b) determining whether the agent binds to said protein.

The present genomic sequences of *Streptococcus pneumoniae* will be of great value to all laboratories working with this organism and for a variety of commercial purposes. Many fragments of the *Streptococcus pneumoniae* genome will be immediately identified by similarity searches against GenBank or protein databases and will be of immediate value to *Streptococcus pneumoniae* researchers

and for immediate commercial value for the production of proteins or to control gene expression.

The methodology and technology for elucidating extensive genomic sequences of bacterial and other genomes has and will greatly enhance the ability to analyze and understand chromosomal organization. In particular, sequenced contigs and genomes will provide the models for developing tools for the analysis of chromosome structure and function, including the ability to identify genes within large segments of genomic DNA, the structure, position, and spacing of regulatory elements, the identification of genes with potential industrial applications, and the ability to do comparative genomic and molecular phylogeny.

DESCRIPTION OF THE FIGURES

FIGURE 1 is a block diagram of a computer system (102) that can be used to implement computer-based systems of present invention.

FIGURE 2 is a schematic diagram depicting the data flow and computer programs used to collect, assemble, edit and annotate the contigs of the *Streptococcus pneumoniae* genome of the present invention. Both Macintosh and Unix platforms are used to handle the AB 373 and 377 sequence data files, largely as described in Kerlavage *et al.*, *Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences*, 585, IEEE Computer Society Press, Washington D.C. (1993). Factura (AB) is a Macintosh program designed for automatic vector sequence removal and end-trimming of sequence files. The program Loadis runs on a Macintosh platform and parses the feature data extracted from the sequence files by Factura to the Unix based *Streptococcus pneumoniae* relational database. Assembly of contigs (and whole genome sequences) is accomplished by retrieving a specific set of sequence files and their associated features using Extrseq, a Unix utility for retrieving sequences from an SQL database. The resulting sequence file is processed by seq_filter to trim portions of the sequences with more than 2% ambiguous nucleotides. The sequence files were assembled using TIGR Assembler, an assembly engine designed at The Institute for Genomic Research (TIGR) for rapid and accurate assembly of thousands of sequence fragments. The collection of contigs generated by the assembly step is loaded into the database with the lassie program. Identification of open reading

frames (ORFs) is accomplished by processing contigs with zorf or GenMark. The ORFs are searched against *S. pneumoniae* sequences from GenBank and against all protein sequences using the BLASTN and BLASTP programs, described in Altschul *et al.*, *J. Mol. Biol. 215:* 403-410 (1990)). Results of the ORF determination and similarity searching steps were loaded into the database. As described below, some results of the determination and the searches are set out in Tables 1-3.

DETAILED DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

The present invention is based on the sequencing of fragments of the *Streptococcus pneumoniae* genome and analysis of the sequences. The primary nucleotide sequences generated by sequencing the fragments are provided in SEQ ID NOS:1-391. (As used herein, the "primary sequence" refers to the nucleotide sequence represented by the IUPAC nomenclature system.)

In addition to the aforementioned *Streptococcus pneumoniae* polynucleotide and polynucleotide sequences, the present invention provides the nucleotide sequences of SEQ ID NOS:1-391, or representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan.

As used herein, a "representative fragment of the nucleotide sequence depicted in SEQ ID NOS:1-391" refers to any portion of the SEQ ID NOS:1-391 which is not presently represented within a publicly available database. Preferred representative fragments of the present invention are *Streptococcus pneumoniae* open reading frames (ORFs), expression modulating fragment (EMFs) and fragments which can be used to diagnose the presence of *Streptococcus pneumoniae* in sample (DFs). A non-limiting identification of preferred representative fragments is provided in Tables 1-3. As discussed in detail below, the information provided in SEQ ID NOS:1-391 and in Tables 1-3 together with routine cloning, synthesis, sequencing and assay methods will enable those skilled in the art to clone and sequence all "representative fragments" of interest, including open reading frames encoding a large variety of *Streptococcus pneumoniae* proteins.

While the presently disclosed sequences of SEQ ID NOS:1-391 are highly accurate, sequencing techniques are not perfect and, in relatively rare instances, further investigation of a fragment or sequence of the invention may reveal a

nucleotide sequence error present in a nucleotide sequence disclosed in SEQ ID NOS:1-391. However, once the present invention is made available (*i.e.*, once the information in SEQ ID NOS:1-391 and Tables 1-3 has been made available), resolving a rare sequencing error in SEQ ID NOS:1-391 will be well within the skill of the art. The present disclosure makes available sufficient sequence information to allow any of the described contigs or portions thereof to be obtained readily by straightforward application of routine techniques. Further sequencing of such polynucleotide may proceed in like manner using manual and automated sequencing methods which are employed ubiquitous in the art. Nucleotide sequence editing software is publicly available. For example, Applied Biosystem's (AB) AutoAssembler can be used as an aid during visual inspection of nucleotide sequences. By employing such routine techniques potential errors readily may be identified and the correct sequence then may be ascertained by targeting further sequencing effort, also of a routine nature, to the region containing the potential error.

Even if all of the very rare sequencing errors in SEQ ID NOS:1-391 were corrected, the resulting nucleotide sequences would still be at least 95% identical, nearly all would be at least 99% identical, and the great majority would be at least 99.9% identical to the nucleotide sequences of SEQ ID NOS:1-391.

As discussed elsewhere herein, polynucleotides of the present invention readily may be obtained by routine application of well known and standard procedures for cloning and sequencing DNA. Detailed methods for obtaining libraries and for sequencing are provided below, for instance. A wide variety of *Streptococcus pneumoniae* strains that can be used to prepare *S. pneumoniae* genomic DNA for cloning and for obtaining polynucleotides of the present invention are available to the public from recognized depository institutions, such as the American Type Culture Collection (ATCC). While the present invention is enabled by the sequences and other information herein disclosed, the *S. pneumoniae* strain that provided the DNA of the present Sequence Listing, Strain 7/87 14.8.91, has been deposited in the ATCC, as a convenience to those of skill in the art. As a further convenience, a library of *S. pneumoniae* genomic DNA, derived from the same strain, also has been deposited in the ATCC. The *S. pneumoniae* strain was deposited on October 10, 1996, and was given Deposit No. 55840, and the cDNA library was deposited on October 11, 1996 and was given Deposit No. 97755. The genomic fragments in the library are 15 to 20 kb

fragments generated by partial Sau3A1 digestion and they are inserted into the BamHI site in the well-known lambda-derived vector lambda DASH II (Stratagene, La Jolla, CA). The provision of the deposits is not a waiver of any rights of the inventors or their assignees in the present subject matter.

The nucleotide sequences of the genomes from different strains of *Streptococcus pneumoniae* differ somewhat. However, the nucleotide sequences of the genomes of all *Streptococcus pneumoniae* strains will be at least 95% identical, in corresponding part, to the nucleotide sequences provided in SEQ ID NOS:1-391. Nearly all will be at least 99% identical and the great majority will be 99.9% identical.

Thus, the present invention further provides nucleotide sequences which are at least 95%, preferably 99% and most preferably 99.9% identical to the nucleotide sequences of SEQ ID NOS:1-391, in a form which can be readily used, analyzed and interpreted by the skilled artisan.

Methods for determining whether a nucleotide sequence is at least 95%, at least 99% or at least 99.9% identical to the nucleotide sequences of SEQ ID NOS:1-391 are routine and readily available to the skilled artisan. For example, the well known fasta algorithm described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA 85:* 2444 (1988) can be used to generate the percent identity of nucleotide sequences. The BLASTN program also can be used to generate an identity score of polynucleotides compared to one another.

COMPUTER RELATED EMBODIMENTS

The nucleotide sequences provided in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a polynucleotide sequence of SEQ ID NOS:1-391 may be "provided" in a variety of mediums to facilitate use thereof. As used herein, provided refers to a manufacture, other than an isolated nucleic acid molecule, which contains a nucleotide sequence of the present invention; *i.e.*, a nucleotide sequence provided in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a polynucleotide of SEQ ID NOS:1-391. Such a manufacture provides a large portion of the *Streptococcus pneumoniae* genome and parts thereof (*e.g.*, a *Streptococcus pneumoniae* open reading frame (ORF)) in a form which allows a skilled artisan to examine the manufacture using

means not directly applicable to examining the *Streptococcus pneumoniae* genome or a subset thereof as it exists in nature or in purified form.

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD- ROM; electrical storage media such as RAM and ROM; and hybrids of these categories, such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. Likewise, it will be clear to those of skill how additional computer readable media that may be developed also can be used to create analogous manufactures having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently know methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention. A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially- available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data-processor structuring formats (*e.g.*, text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. Thus, by providing in computer readable form the nucleotide sequences of SEQ ID NOS:1-

391, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a sequence of SEQ ID NOS:1-391 the present invention enables the skilled artisan routinely to access the provided sequence information for a wide variety of purposes.

The examples which follow demonstrate how software which implements the BLAST (Altschul *et al.*, *J. Mol. Biol. 215*:403-410 (1990)) and BLAZE (Brutlag *et al.*, *Comp. Chem. 17*:203-207 (1993)) search algorithms on a Sybase system was used to identify open reading frames (ORFs) within the *Streptococcus pneumoniae* genome which contain homology to ORFs or proteins from both *Streptococcus pneumoniae* and from other organisms. Among the ORFs discussed herein are protein encoding fragments of the *Streptococcus pneumoniae* genome useful in producing commercially important proteins, such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify, among other things, commercially important fragments of the *Streptococcus pneumoniae* genome.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention.

As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means.

As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage

means. Search means are used to identify fragments or regions of the present genomic sequences which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, MacPattern (EMBL), BLASTN and BLASTX (NCBIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *Streptococcus pneumoniae* genomic sequences possessing varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the

Streptococcus pneumoniae genome. In the present examples, implementing software which implement the BLAST and BLAZE algorithms, described in Altschul *et al., J. Mol. Biol. 215:* 403-410 (1990), is used to identify open reading frames within the *Streptococcus pneumoniae* genome. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention. Of course, suitable proprietary systems that may be known to those of skill also may be employed in this regard.

Figure 1 provides a block diagram of a computer system illustrative of embodiments of this aspect of present invention. The computer system 102 includes a processor 106 connected to a bus 104. Also connected to the bus 104 are a main memory 108 (preferably implemented as random access memory, RAM) and a variety of secondary storage devices 110, such as a hard drive 112 and a removable medium storage device 114. The removable medium storage device 114 may represent, for example, a floppy disk drive, a CD-ROM drive, a magnetic tape drive, *etc.* A removable storage medium 116 (such as a floppy disk, a compact disk, a magnetic tape, *etc.*) containing control logic and/or data recorded therein may be inserted into the removable medium storage device 114. The computer system 102 includes appropriate software for reading the control logic and/or the data from the removable medium storage device 114, once it is inserted into the removable medium storage device 114.

A nucleotide sequence of the present invention may be stored in a well known manner in the main memory 108, any of the secondary storage devices 110, and/or a removable storage medium 116. During execution, software for accessing and processing the genomic sequence (such as search tools, comparing tools, *etc.*) reside in main memory 108, in accordance with the requirements and operating parameters of the operating system, the hardware system and the software program or programs.

BIOCHEMICAL EMBODIMENTS

Other embodiments of the present invention are directed to isolated fragments of the *Streptococcus pneumoniae* genome. The fragments of the *Streptococcus pneumoniae* genome of the present invention include, but are not limited to fragments which encode peptides and polypeptides, hereinafter open reading frames (ORFs), fragments which modulate the expression of an operably linked ORF, hereinafter expression modulating fragments (EMFs) and fragments which can be used to diagnose the presence of *Streptococcus pneumoniae* in a sample, hereinafter diagnostic fragments (DFs).

As used herein, an "isolated nucleic acid molecule" or an "isolated fragment of the *Streptococcus pneumoniae* genome" refers to a nucleic acid molecule possessing a specific nucleotide sequence which has been subjected to purification means to reduce, from the composition, the number of compounds which are normally associated with the composition. Particularly, the term refers to the nucleic acid molecules having the sequences set out in SEQ ID NOS:1-391, to representative fragments thereof as described above, to polynucleotides at least 95%, preferably at least 99% and especially preferably at least 99.9% identical in sequence thereto, also as set out above.

A variety of purification means can be used to generate the isolated fragments of the present invention. These include, but are not limited to methods which separate constituents of a solution based on charge, solubility, or size.

In one embodiment, *Streptococcus pneumoniae* DNA can be enzymatically sheared to produce fragments of 15-20 kb in length. These fragments can then be used to generate a *Streptococcus pneumoniae* library by inserting them into lambda clones as described in the Examples below. Primers flanking, for example, an ORF, such as those enumerated in Tables 1-3 can then be generated using nucleotide sequence information provided in SEQ ID NOS:1-391. Well known and routine techniques of PCR cloning then can be used to isolate the ORF from the lambda DNA library or *Streptococcus pneumoniae* genomic DNA. Thus, given the availability of SEQ ID NOS:1-391, the information in Tables 1, 2 and 3, and the information that may be obtained readily by analysis of the sequences of SEQ ID NOS:1-391 using methods set out above, those of skill will be enabled by the present disclosure to isolate any ORF-containing or other nucleic acid fragment of the present invention.

The isolated nucleic acid molecules of the present invention include, but are not limited to single stranded and double stranded DNA, and single stranded RNA.

As used herein, an "open reading frame," ORF, means a series of triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

Tables 1, 2, and 3 list ORFs in the *Streptococcus pneumoniae* genomic contigs of the present invention that were identified as putative coding regions by the GeneMark software using organism-specific second-order Markov probability transition matrices. It will be appreciated that other criteria can be used, in accordance with well known analytical methods, such as those discussed herein, to generate more inclusive, more restrictive, or more selective lists.

Table 1 sets out ORFs in the *Streptococcus pneumoniae* contigs of the present invention that over a continuous region of at least 50 bases are 95% or more identical (by BLAST analysis) to a nucleotide sequence available through GenBank in October, 1997.

Table 2 sets out ORFs in the *Streptococcus pneumoniae* contigs of the present invention that are not in Table 1 and match, with a BLASTP probability score of 0.01 or less, a polypeptide sequence available through GenBank in October, 1997.

Table 3 sets out ORFs in the *Streptococcus pneumoniae* contigs of the present invention that do not match significantly, by BLASTP analysis, a polypeptide sequence available through GenBank in October, 1997.

In each table, the first and second columns identify the ORF by, respectively, contig number and ORF number within the contig; the third column indicates the first nucleotide of the ORF (actually the first nucleotide of the stop codon immediately preceeding the ORF), counting from the 5' end of the contig strand; and the fourth column, "stop (nt)" indicates the last nucleotide of the stop codon defining the 3'end of the ORF.

In Tables 1 and 2, column five, lists the Reference for the closest matching sequence available through GenBank. These reference numbers are the databases entry numbers commonly used by those of skill in the art, who will be familiar with their denominators. Descriptions of the nomenclature are available from the National Center for Biotechnology Information. Column six in Tables 1 and 2 provides the gene name of the matching sequence; column seven provides the BLAST identity score and column eight the BLAST similarity score from the

comparison of the ORF and the homologous gene; and column nine indicates the length in nucleotides of the highest scoring segment pair identified by the BLAST identity analysis.

Each ORF described in the tables is defined by "start (nt)" (5') and "stop (nt)" (3') nucleotide position numbers. These position numbers refer to the boundaries of each ORF and provide orientation with respect to whether the forward or reverse strand is the coding strand and which reading frame the coding sequence is contained. The "start" position is the first nucleotide of the triplet encoding a stop codon just 5' to the ORF and the "stop" position is the last nucleotide of the triplet encoding the next in-frame stop codon (i.e., the stop codon at the 3' end of the ORF). Those of ordinary skill in the art appreciate that preferred fragments within each ORF described in the table include fragments of each ORF which include the entire sequence from the delineated "start" and "stop" positions excepting the first and last three nucleotides since these encode stop codons. Thus, polynucleotides set out as ORFs in the tables but lacking the three (3) 5' nucleotides and the three (3) 3' nucleotides are encompassed by the present invention. Those of skill also appreciate that particularly preferred are fragments within each ORF that are polynucleotide fragments comprising polypeptide coding sequence. As defined herein, "coding sequence" includes the fragment within an ORF beginning at the first in-frame ATG (triplet encoding methionine) and ending with the last nucleotide prior to the triplet encoding the 3' stop codon. Preferred are fragments comprising the entire coding sequence and fragments comprising the entire coding sequence, excepting the coding sequence for the N-terminal methionine. Those of skill appreciate that the N-terminal methionine is often removed during post-translational processing and that polynucleotides lacking the ATG can be used to facilitate production of N-termainal fusion proteins which may be benefical in the production or use of genetically engineered proteins. Of course, due to the degeneracy of the genetic code many polynucleotides can encode a given polypeptide. Thus, the invention further includes polynucleotides comprising a nucleotide sequence encoding a polypeptide sequence itself encoded by the coding sequence within an ORF described in Tables 1-3 herein. Further, polynucleotides at least 95%, preferably at least 99% and especially preferably at least 99.9% identical in sequence to the foregoing polynucleotides, are contemplated by the present invention.

Polypeptides encoded by polynucleotides described above and elsewhere herein are also provided by the present invention as are polypeptide comprising a an amino acid sequence at least about 95%, preferably at least 97% and even more preferably 99% identical to the amino acid sequence of a polypeptide encoded by an ORF shown in Tables 1-3. These polypeptides may or may not comprise an N-terminal methionine.

The concepts of percent identity and percent similarity of two polypeptide sequences is well understood in the art. For example, two polypeptides 10 amino acids in length which differ at three amino acid positions (*e.g.*, at positions 1, 3 and 5) are said to have a percent identity of 70%. However, the same two polypeptides would be deemed to have a percent similarity of 80% if, for example at position 5, the amino acids moieties, although not identical, were "similar" (*i.e.*, possessed similar biochemical characteristics). Many programs for analysis of nucleotide or amino acid sequence similarity, such as fasta and BLAST specifically list percent identity of a matching region as an output parameter. Thus, for instance, Tables 1 and 2 herein enumerate the percent identity of the highest scoring segment pair in each ORF and its listed relative. Further details concerning the algorithms and criteria used for homology searches are provided below and are described in the pertinent literature highlighted by the citations provided below.

It will be appreciated that other criteria can be used to generate more inclusive and more exclusive listings of the types set out in the tables. As those of skill will appreciate, narrow and broad searches both are useful. Thus, a skilled artisan can readily identify ORFs in contigs of the *Streptococcus pneumoniae* genome other than those listed in Tables 1-3, such as ORFs which are overlapping or encoded by the opposite strand of an identified ORF in addition to those ascertainable using the computer-based systems of the present invention.

As used herein, an "expression modulating fragment," EMF, means a series of nucleotide molecules which modulates the expression of an operably linked ORF or EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are fragments which induce the expression or an operably linked ORF in response to a specific regulatory factor or physiological event.

EMF sequences can be identified within the contigs of the *Streptococcus pneumoniae* genome by their proximity to the ORFs provided in Tables 1-3. An intergenic segment, or a fragment of the intergenic segment, from about 10 to 200 nucleotides in length, taken from any one of the ORFs of Tables 1-3 will modulate the expression of an operably linked ORF in a fashion similar to that found with the naturally linked ORF sequence. As used herein, an "intergenic segment" refers to fragments of the *Streptococcus pneumoniae* genome which are between two ORF(s) herein described. EMFs also can be identified using known EMFs as a target sequence or target motif in the computer-based systems of the present invention. Further, the two methods can be combined and used together.

The presence and activity of an EMF can be confirmed using an EMF trap vector. An EMF trap vector contains a cloning site linked to a marker sequence. A marker sequence encodes an identifiable phenotype, such as antibiotic resistance or a complementing nutrition auxotrophic factor, which can be identified or assayed when the EMF trap vector is placed within an appropriate host under appropriate conditions. As described above, a EMF will modulate the expression of an operably linked marker sequence. A more detailed discussion of various marker sequences is provided below. A sequence which is suspected as being an EMF is cloned in all three reading frames in one or more restriction sites upstream from the marker sequence in the EMF trap vector. The vector is then transformed into an appropriate host using known procedures and the phenotype of the transformed host in examined under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence.

As used herein, a "diagnostic fragment," DF, means a series of nucleotide molecules which selectively hybridize to *Streptococcus pneumoniae* sequences. DFs can be readily identified by identifying unique sequences within contigs of the *Streptococcus pneumoniae* genome, such as by using well-known computer analysis software, and by generating and testing probes or amplification primers

consisting of the DF sequence in an appropriate diagnostic format which determines amplification or hybridization selectivity.

The sequences falling within the scope of the present invention are not limited to the specific sequences herein described, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequences provided in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95%, preferrably at least 99% and most at least preferably 99.9% identical to SEQ ID NOS:1-391, with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another which encodes the same amino acid is expressly contemplated. Any specific sequence disclosed herein can be readily screened for errors by resequencing a particular fragment, such as an ORF, in both directions (*i.e.*, sequence both strands). Alternatively, error screening can be performed by sequencing corresponding polynucleotides of *Streptococcus pneumoniae* origin isolated by using part or all of the fragments in question as a probe or primer.

Preferred DFs of the present invention comprise at least about 17, preferrably at least about 20, and more preferrably at least about 50 contiguous nucleotides within an ORF set out in Tables 1-3. Most highly preferred DFs specifically hybridize to a polynucleotide containing the sequence of the ORF from which they are derived. Specific hybridization occurs even under stringent conditions defined elsewhere herein.

Each of the ORFs of the *Streptococcus pneumoniae* genome disclosed in Tables 1, 2 and 3, and the EMFs found 5' to the ORFs, can be used as polynucleotide reagents in numerous ways. For example, the sequences can be used as diagnostic probes or diagnostic amplification primers to detect the presence of a specific microbe in a sample, particularly *Streptococcus pneumoniae*. Especially preferred in this regard are ORFs such as those of Table 3, which do not match previously characterized sequences from other organisms and thus are most likely to be highly selective for *Streptococcus pneumoniae*. Also particularly preferred are ORFs that can be used to distinguish between strains of *Streptococcus pneumoniae*, particularly those that distinguish medically important strain, such as drug-resistant strains.

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Information from the sequences of the present invention can be used to design antisense and triple helix-forming oligonucleotides. Polynucleotides suitable for use in these methods are usually 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription, for triple-helix formation, or to the mRNA itself, for antisense inhibition. Both techniques have been demonstrated to be effective in model systems, and the requisite techniques are well known and involve routine procedures. Triple helix techniques are discussed in, for example, Lee *et al.*, *Nucl. Acids Res. 6*:3073 (1979); Cooney *et al.*, *Science 241*:456 (1988); and Dervan *et al.*, *Science 251*:1360 (1991). Antisense techniques in general are discussed in, for instance, Okano, *J. Neurochem. 56*:560 (1991) and *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)).

The present invention further provides recombinant constructs comprising one or more fragments of the *Streptococcus pneumoniae* genomic fragments and contigs of the present invention. Certain preferred recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a fragment of the *Streptococcus pneumoniae* genome has been inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. For vectors comprising the EMFs of the present invention, the vector may further comprise a marker sequence or heterologous ORF operably linked to the EMF.

Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Useful bacterial vectors include phagescript, PsiX174, pBluescript SK, pBS KS, pNH8a, pNH16a, pNH18a, pNH46a (available from Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (available from Pharmacia). Useful eukaryotic vectors include pWLneo, pSV2cat, pOG44, pXT1, pSG

(available from Stratagene) pSVK3, pBPV, pMSG, pSVL (available from Pharmacia).

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein- I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

The present invention further provides host cells containing any one of the isolated fragments of the *Streptococcus pneumoniae* genomic fragments and contigs of the present invention, wherein the fragment has been introduced into the host cell using known methods. The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or a procaryotic cell, such as a bacterial cell.

A polynucleotide of the present invention, such as a recombinant construct comprising an ORF of the present invention, may be introduced into the host by a variety of well established techniques that are standard in the art, such as calcium phosphate transfection, DEAE, dextran mediated transfection and electroporation, which are described in, for instance, Davis, L. *et al.*, BASIC METHODS IN MOLECULAR BIOLOGY (1986).

A host cell containing one of the fragments of the *Streptococcus pneumoniae* genomic fragments and contigs of the present invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF. The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the Genetic Code, encode an identical polypeptide sequence.

Preferred nucleic acid fragments of the present invention are the ORFs and subfragments thereof depicted in Tables 2 and 3 which encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. This is particularly useful in producing small peptides and fragments of larger polypeptides. Such short fragments as may be obtained most readily by synthesis are useful, for example, in generating antibodies against the native polypeptide, as discussed further below.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily employ well-known methods for isolating polypeptides and proteins to isolate and purify polypeptides or proteins of the present invention produced naturally by a bacterial strain, or by other methods. Methods for isolation and purification that can be employed in this regard include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography.

The polypeptides and proteins of the present invention also can be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. Those skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, CV-1 cell, COS cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level.

"Recombinant," as used herein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial"defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern different from that expressed in mammalian cells.

"Nucleotide sequence" refers to a heteropolymer of deoxyribonucleotides. Generally, DNA segments encoding the polypeptides and proteins provided by this invention are assembled from fragments of the *Streptococcus pneumoniae* genome and short oligonucleotide linkers, or from a series of oligonucleotides, to provide a synthetic gene which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon.

Recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. The expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic regulatory elements necessary for gene expression in the host, including elements required to initiate and maintain transcription at a level sufficient for suitable expression of the desired polypeptide, including, for example, promoters and, where necessary, an enhancer and a polyadenylation signal; (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate signals to initiate translation at the beginning of the desired coding region and terminate translation at its end. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an N-terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

"Recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extra chromosomally. The cells can be prokaryotic or eukaryotic. Recombinant expression systems as defined herein will express

heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed.

Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual,* 2nd Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference in its entirety.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3- phosphoglycerate kinase (PGK), alpha-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and, when desirable, provide amplification within the host.

Suitable prokaryotic hosts for transformation include strains of *E. coli*, *B. subtilis, Salmonella typhimurium* and various species within the genera *Pseudomonas* and *Streptomyces*. Others may, also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication

derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (available form Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (available from Promega Biotec, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter, where it is inducible, is derepressed or induced by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period to provide for expression of the induced gene product. Thereafter cells are typically harvested, generally by centrifugation, disrupted to release expressed protein, generally by physical or chemical means, and the resulting crude extract is retained for further purification.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described in Gluzman, *Cell 23:*175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines.

Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

Recombinant polypeptides and proteins produced in bacterial culture is usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The present invention further includes isolated polypeptides, proteins and nucleic acid molecules which are substantially equivalent to those herein described. As used herein, substantially equivalent can refer both to nucleic acid and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between reference and subject sequences. For purposes of the present invention, sequences having equivalent biological activity, and equivalent expression characteristics are considered substantially equivalent. For purposes of determining equivalence, truncation of the mature sequence should be disregarded.

The invention further provides methods of obtaining homologs from other strains of *Streptococcus pneumoniae*, of the fragments of the *Streptococcus pneumoniae* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. As used herein, a sequence or protein of *Streptococcus pneumoniae* is defined as a homolog of a fragment of the *Streptococcus pneumoniae* fragments or contigs or a protein encoded by one of the ORFs of the present invention, if it shares significant homology to one of the fragments of the *Streptococcus pneumoniae* genome of the present invention or a protein encoded by one of the ORFs of the present invention. Specifically, by using the sequence disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

As used herein, two nucleic acid molecules or proteins are said to "share significant homology" if the two contain regions which possess greater than 85% sequence (amino acid or nucleic acid) homology. Preferred homologs in this regard are those with more than 90% homology. Especially preferred are those with 93% or more homology. Among especially preferred homologs those with 95% or more homology are particularly preferred. Very particularly preferred among these are those with 97% and even more particularly preferred among those are homologs with 99% or more homology. The most preferred homologs among these are those with 99.9% homology or more. It will be understood that, among measures of homology, identity is particularly preferred in this regard.

Region specific primers or probes derived from the nucleotide sequence provided in SEQ ID NOS:1-391 or from a nucleotide sequence at least 95%, particularly at least 99%, especially at least 99.5% identical to a sequence of SEQ

ID NOS:1-391 can be used to prime DNA synthesis and PCR amplification, as well as to identify colonies containing cloned DNA encoding a homolog. Methods suitable to this aspect of the present invention are well known and have been described in great detail in many publications such as, for example, Innis *et al.*, *PCR Protocols*, Academic Press, San Diego, CA (1990)).

When using primers derived from SEQ ID NOS:1-391 or from a nucleotide sequence having an aforementioned identity to a sequence of SEQ ID NOS:1-391, one skilled in the art will recognize that by employing high stringency conditions (*e.g.*, annealing at 50-60°C in 6X SSPC and 50% formamide, and washing at 50-65°C in 0.5X SSPC) only sequences which are greater than 75% homologous to the primer will be amplified. By employing lower stringency conditions (*e.g.*, hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequences which are greater than 40-50% homologous to the primer will also be amplified.

When using DNA probes derived from SEQ ID NOS:1-391, or from a nucleotide sequence having an aforementioned identity to a sequence of SEQ ID NOS:1-391, for colony/plaque hybridization, one skilled in the art will recognize that by employing high stringency conditions (*e.g.*, hybridizing at 50- 65°C in 5X SSPC and 50% formamide, and washing at 50- 65°C in 0.5X SSPC), sequences having regions which are greater than 90% homologous to the probe can be obtained, and that by employing lower stringency conditions (*e.g.*, hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequences having regions which are greater than 35-45% homologous to the probe will be obtained.

Any organism can be used as the source for homologs of the present invention so long as the organism naturally expresses such a protein or contains genes encoding the same. The most preferred organism for isolating homologs are bacteria which are closely related to *Streptococcus pneumoniae*.

ILLUSTRATIVE USES OF COMPOSITIONS OF THE INVENTION

Each ORF provided in Tables 1 and 2 is identified with a function by homology to a known gene or polypeptide. As a result, one skilled in the art can use the polypeptides of the present invention for commercial, therapeutic and industrial purposes consistent with the type of putative identification of the

polypeptide. Such identifications permit one skilled in the art to use the *Streptococcus pneumoniae* ORFs in a manner similar to the known type of sequences for which the identification is made; for example, to ferment a particular sugar source or to produce a particular metabolite. A variety of reviews illustrative of this aspect of the invention are available, including the following reviews on the industrial use of enzymes, for example, BIOCHEMICAL ENGINEERING AND BIOTECHNOLOGY HANDBOOK, 2nd Ed., MacMillan Publications, Ltd. NY (1991) and BIOCATALYSTS IN ORGANIC SYNTHESES, Tramper *et al.*, Eds., Elsevier Science Publishers, Amsterdam, The Netherlands (1985). A variety of exemplary uses that illustrate this and similar aspects of the present invention are discussed below.

1. Biosynthetic Enzymes

Open reading frames encoding proteins involved in mediating the catalytic reactions involved in intermediary and macromolecular metabolism, the biosynthesis of small molecules, cellular processes and other functions includes enzymes involved in the degradation of the intermediary products of metabolism, enzymes involved in central intermediary metabolism, enzymes involved in respiration, both aerobic and anaerobic, enzymes involved in fermentation, enzymes involved in ATP proton motor force conversion, enzymes involved in broad regulatory function, enzymes involved in amino acid synthesis, enzymes involved in nucleotide synthesis, enzymes involved in cofactor and vitamin synthesis, can be used for industrial biosynthesis.

The various metabolic pathways present in *Streptococcus pneumoniae* can be identified based on absolute nutritional requirements as well as by examining the various enzymes identified in Table 1-3 and SEQ ID NOS:1-391.

Of particular interest are polypeptides involved in the degradation of intermediary metabolites as well as non-macromolecular metabolism. Such enzymes include amylases, glucose oxidases, and catalase.

Proteolytic enzymes are another class of commercially important enzymes. Proteolytic enzymes find use in a number of industrial processes including the processing of flax and other vegetable fibers, in the extraction, clarification and depectinization of fruit juices, in the extraction of vegetables' oil and in the maceration of fruits and vegetables to give unicellular fruits. A detailed review of the proteolytic enzymes used in the food industry is provided in Rombouts *et al.*,

*Symbiosis 21:*79 (1986) and Voragen *et al.* in *Biocatalysts In Agricultural Biotechnology*, Whitaker *et al.*, Eds., *American Chemical Society Symposium Series 389*:93 (1989) .

The metabolism of sugars is an important aspect of the primary metabolism of *Streptococcus pneumoniae*. Enzymes involved in the degradation of sugars, such as, particularly, glucose, galactose, fructose and xylose, can be used in industrial fermentation. Some of the important sugar transforming enzymes, from a commercial viewpoint, include sugar isomerases such as glucose isomerase. Other metabolic enzymes have found commercial use such as glucose oxidases which produces ketogulonic acid (KGA). KGA is an intermediate in the commercial production of ascorbic acid using the Reichstein's procedure, as described in Krueger *et al., Biotechnology* 6(A), Rhine *et al.*, Eds., Verlag Press, Weinheim, Germany (1984).

Glucose oxidase (GOD) is commercially available and has been used in purified form as well as in an immobilized form for the deoxygenation of beer. See, for instance, Hartmeir *et al.*, *Biotechnology Letters 1*:21 (1979). The most important application of GOD is the industrial scale fermentation of gluconic acid. Market for gluconic acids which are used in the detergent, textile, leather, photographic, pharmaceutical, food, feed and concrete industry, as described, for example, in Bigelis *et al.*, beginning on page 357 in GENE MANIPULATIONS AND FUNGI; Benett *et al.*, Eds., Academic Press, New York (1985). In addition to industrial applications, GOD has found applications in medicine for quantitative determination of glucose in body fluids recently in biotechnology for analyzing syrups from starch and cellulose hydrosylates. This application is described in Owusu *et al.*, *Biochem. et Biophysica. Acta. 872:*83 (1986), for instance.

The main sweetener used in the world today is sugar which comes from sugar beets and sugar cane. In the field of industrial enzymes, the glucose isomerase process shows the largest expansion in the market today. Initially, soluble enzymes were used and later immobilized enzymes were developed (Krueger *et al.*, *Biotechnology, The Textbook of Industrial Microbiology*, Sinauer Associated Incorporated, Sunderland, Massachusetts (1990)). Today, the use of glucose- produced high fructose syrups is by far the largest industrial business using immobilized enzymes. A review of the industrial use of these enzymes is provided by Jorgensen, Starch *40*:307 (1988).

Proteinases, such as alkaline serine proteinases, are used as detergent additives and thus represent one of the largest volumes of microbial enzymes used in the industrial sector. Because of their industrial importance, there is a large body of published and unpublished information regarding the use of these enzymes in industrial processes. (See Faultman *et al.*, Acid Proteases Structure Function and Biology, Tang, J., ed., Plenum Press, New York (1977) and Godfrey *et al.*, Industrial Enzymes, MacMillan Publishers, Surrey, UK (1983) and Hepner *et al.*, Report Industrial Enzymes by 1990, Hel Hepner & Associates, London (1986)).

Another class of commercially usable proteins of the present invention are the microbial lipases, described by, for instance, Macrae *et al.*, *Philosophical Transactions of the Chiral Society of London 310*:227 (1985) and Poserke, *Journal of the American Oil Chemist Society 61:*1758 (1984). A major use of lipases is in the fat and oil industry for the production of neutral glycerides using lipase catalyzed inter-esterification of readily available triglycerides. Application of lipases include the use as a detergent additive to facilitate the removal of fats from fabrics in the course of the washing procedures.

The use of enzymes, and in particular microbial enzymes, as catalyst for key steps in the synthesis of complex organic molecules is gaining popularity at a great rate. One area of great interest is the preparation of chiral intermediates. Preparation of chiral intermediates is of interest to a wide range of synthetic chemists particularly those scientists involved with the preparation of new pharmaceuticals, agrochemicals, fragrances and flavors. (See Davies *et al.*, *Recent Advances in the Generation of Chiral Intermediates Using Enzymes*, CRC Press, Boca Raton, Florida (1990)). The following reactions catalyzed by enzymes are of interest to organic chemists: hydrolysis of carboxylic acid esters, phosphate esters, amides and nitriles, esterification reactions, trans-esterification reactions, synthesis of amides, reduction of alkanones and oxoalkanates, oxidation of alcohols to carbonyl compounds, oxidation of sulfides to sulfoxides, and carbon bond forming reactions such as the aldol reaction.

When considering the use of an enzyme encoded by one of the ORFs of the present invention for biotransformation and organic synthesis it is sometimes necessary to consider the respective advantages and disadvantages of using a microorganism as opposed to an isolated enzyme. Pros and cons of using a whole cell system on the one hand or an isolated partially purified enzyme on the other

hand, has been described in detail by Bud *et al.*, Chemistry in Britain (1987), p. 127.

Amino transferases, enzymes involved in the biosynthesis and metabolism of amino acids, are useful in the catalytic production of amino acids. The advantages of using microbial based enzyme systems is that the amino transferase enzymes catalyze the stereo- selective synthesis of only L-amino acids and generally possess uniformly high catalytic rates. A description of the use of amino transferases for amino acid production is provided by Roselle-David, *Methods of Enzymology 136*:479 (1987).

Another category of useful proteins encoded by the ORFs of the present invention include enzymes involved in nucleic acid synthesis, repair, and recombination.

2. Generation of Antibodies

As described here, the proteins of the present invention, as well as homologs thereof, can be used in a variety of procedures and methods known in the art which are currently applied to other proteins. The proteins of the present invention can further be used to generate an antibody which selectively binds the protein. Such antibodies can be either monoclonal or polyclonal antibodies, as well fragments of these antibodies, and humanized forms.

The invention further provides antibodies which selectively bind to one of the proteins of the present invention and hybridomas which produce these antibodies. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing polyclonal and monoclonal antibodies as well as hybridomas capable of producing the desired antibody are well known in the art (Campbell, A. M., *Monoclonal Antibody Technology: Laboratory Techniques In Biochemistry And Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth *et al.*, *J. Immunol. Methods 35:* 1-21 (1980), Kohler and Milstein, *Nature 256:*495-497 (1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, *Immunology Today 4:*72 (1983), pgs. 77-96 of Cole *et al.*, in *Monoclonal Antibodies And Cancer Therapy*, Alan R. Liss, Inc. (1985)). Any animal (mouse, rabbit, *etc.*) which is known to produce antibodies can be immunized with the pseudogene polypeptide. Methods for immunization are well known in the art. Such methods

include subcutaneous or interperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of the protein encoded by the ORF of the present invention used for immunization will vary based on the animal which is immunized, the antigenicity of the peptide and the site of injection.

The protein which is used as an immunogen may be modified or administered in an adjuvant in order to increase the protein's antigenicity. Methods of increasing the antigenicity of a protein are well known in the art and include, but are not limited to coupling the antigen with a heterologous protein (such as globulin or galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells.

Any one of a number of methods well known in the art can be used to identify the hybridoma cell which produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al.*, *Exp. Cell Res. 175:*109-124 (1988)).

Hybridomas secreting the desired antibodies are cloned and the class and subclass is determined using procedures known in the art (Campbell, A. M., *Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1984)).

Techniques described for the production of single chain antibodies (U. S. Patent 4,946,778) can be adapted to produce single chain antibodies to proteins of the present invention.

For polyclonal antibodies, antibody containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures.

The present invention further provides the above- described antibodies in detectably labelled form. Antibodies can be detectably labelled through the use of radioisotopes, affinity labels (such as biotin, avidin, *etc.*), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase, *etc.*) fluorescent labels (such as FITC or rhodamine, *etc.*), paramagnetic atoms, *etc.* Procedures for accomplishing such labeling are well-known in the art, for example see Sternberger *et al.*, *J. Histochem. Cytochem. 18:*315 (1970); Bayer, E. A. *et al.*, *Meth. Enzym. 62*:308

(1979); Engval, E. *et al.*, *Immunol. 109*:129 (1972); Goding, J. W., *J. Immunol. Meth. 13:*215 (1976)).

The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and in situ assays to identify cells or tissues in which a fragment of the *Streptococcus pneumoniae* genome is expressed.

The present invention further provides the above-described antibodies immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir, D. M. *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10 (1986); Jacoby, W. D. *et al.*, Meth. Enzym. 34 Academic Press, N. Y. (1974)). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and in situ assays as well as for immunoaffinity purification of the proteins of the present invention.

3. Diagnostic Assays and Kits

The present invention further provides methods to identify the expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using one of the DFs or antibodies of the present invention.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the DFs of the present invention and assaying for binding of the DFs or antibodies to components within the test sample.

Conditions for incubating a DF or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the DF or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the DFs or antibodies of the present invention. Examples of such assays can be found in Chard, T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G. R. *et al.*, *Techniques in Immunocytochemistry,* Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and*

Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985).

The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the DFs or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound DF or antibody.

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, *etc.*), and containers which contain the reagents used to detect the bound antibody or DF.

Types of detection reagents include labelled nucleic acid probes, labelled secondary antibodies, or in the alternative, if the primary antibody is labelled, the enzymatic, or antibody binding reagents which are capable of reacting with the labelled antibody. One skilled in the art will readily recognize that the disclosed DFs and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4. Screening Assay for Binding Agents

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents which bind to a protein encoded by one of the ORFs of the present invention or to one of the fragments and the *Streptococcus pneumoniae* fragment and contigs herein described.

In general, such methods comprise steps of:

(a) contacting an agent with an isolated protein encoded by one of the ORFs of the present invention, or an isolated fragment of the *Streptococcus pneumoniae* genome; and

(b) determining whether the agent binds to said protein or said fragment.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention.

Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides, for example see Hurby *et al.*, "Application of Synthetic Peptides: Antisense Peptides," in *Synthetic Peptides, A User's Guide*, W. H. Freeman, NY (1992), pp. 289-307, and Kaspczak *et al.*, *Biochemistry 28:*9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control.

One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods usually contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, *Nucl. Acids Res. 6*:3073 (1979); Cooney *et al.*, *Science 241*:456 (1988); and Dervan *et al.*, *Science 251:*1360 (1991)) or to the mRNA itself (antisense - Okano, *J. Neurochem. 56:*560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression,* CRC Press, Boca Raton, FL (1988)). Triple helix- formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention can be used to design antisense and triple helix-forming oligonucleotides, and other DNA binding agents.

5. Pharmaceutical Compositions and Vaccines

The present invention further provides pharmaceutical agents which can be used to modulate the growth or pathogenicity of *Streptococcus pneumoniae*, or another related organism, *in vivo* or *in vitro*. As used herein, a "pharmaceutical agent" is defined as a composition of matter which can be formulated using known techniques to provide a pharmaceutical compositions. As used herein, the "pharmaceutical agents of the present invention" refers the pharmaceutical agents which are derived from the proteins encoded by the ORFs of the present invention or are agents which are identified using the herein described assays.

As used herein, a pharmaceutical agent is said to "modulate the growth pathogenicity of *Streptococcus pneumoniae* or a related organism, *in vivo* or *in vitro*," when the agent reduces the rate of growth, rate of division, or viability of the organism in question. The pharmaceutical agents of the present invention can modulate the growth or pathogenicity of an organism in many fashions, although an understanding of the underlying mechanism of action is not needed to practice the use of the pharmaceutical agents of the present invention. Some agents will modulate the growth by binding to an important protein thus blocking the biological activity of the protein, while other agents may bind to a component of the outer

surface of the organism blocking attachment or rendering the organism more prone to act the bodies nature immune system. Alternatively, the agent may comprise a protein encoded by one of the ORFs of the present invention and serve as a vaccine. The development and use of a vaccine based on outer membrane components are well known in the art.

As used herein, a "related organism" is a broad term which refers to any organism whose growth can be modulated by one of the pharmaceutical agents of the present invention. In general, such an organism will contain a homolog of the protein which is the target of the pharmaceutical agent or the protein used as a vaccine. As such, related organisms do not need to be bacterial but may be fungal or viral pathogens.

The pharmaceutical agents and compositions of the present invention may be administered in a convenient manner, such as by the oral, topical, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes. The pharmaceutical compositions are administered in an amount which is effective for treating and/or prophylaxis of the specific indication. In general, they are administered in an amount of at least about 1 mg/kg body weight and in most cases they will be administered in an amount not in excess of about 1 g/kg body weight per day. In most cases, the dosage is from about 0.1 mg/kg to about 10 g/kg body weight daily, taking into account the routes of administration, symptoms, *etc.*

The agents of the present invention can be used in native form or can be modified to form a chemical derivative. As used herein, a molecule is said to be a "chemical derivative" of another molecule when it contains additional chemical moieties not normally a part of the molecule. Such moieties may improve the molecule's solubility, absorption, biological half life, *etc.* The moieties may alternatively decrease the toxicity of the molecule, eliminate or attenuate any undesirable side effect of the molecule, *etc.* Moieties capable of mediating such effects are disclosed in, among other sources, REMINGTON'S PHARMACEUTICAL SCIENCES (1980) cited elsewhere herein.

For example, such moieties may change an immunological character of the functional derivative, such as affinity for a given antibody. Such changes in immunomodulation activity are measured by the appropriate assay, such as a competitive type immunoassay. Modifications of such protein properties as redox or thermal stability, biological half-life, hydrophobicity, susceptibility to proteolytic degradation or the tendency to aggregate with carriers or into multimers also may

be effected in this way and can be assayed by methods well known to the skilled artisan.

The therapeutic effects of the agents of the present invention may be obtained by providing the agent to a patient by any suitable means (*e.g.*, inhalation, intravenously, intramuscularly, subcutaneously, enterally, or parenterally). It is preferred to administer the agent of the present invention so as to achieve an effective concentration within the blood or tissue in which the growth of the organism is to be controlled. To achieve an effective blood concentration, the preferred method is to administer the agent by injection. The administration may be by continuous infusion, or by single or multiple injections.

In providing a patient with one of the agents of the present invention, the dosage of the administered agent will vary depending upon such factors as the patient's age, weight, height, sex, general medical condition, previous medical history, *etc.* In general, it is desirable to provide the recipient with a dosage of agent which is in the range of from about 1 pg/kg to 10 mg/kg (body weight of patient), although a lower or higher dosage may be administered. The therapeutically effective dose can be lowered by using combinations of the agents of the present invention or another agent.

As used herein, two or more compounds or agents are said to be administered "in combination" with each other when either (1) the physiological effects of each compound, or (2) the serum concentrations of each compound can be measured at the same time. The composition of the present invention can be administered concurrently with, prior to, or following the administration of the other agent.

The agents of the present invention are intended to be provided to recipient subjects in an amount sufficient to decrease the rate of growth (as defined above) of the target organism.

The administration of the agent(s) of the invention may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically, the agent(s) are provided in advance of any symptoms indicative of the organisms growth. The prophylactic administration of the agent(s) serves to prevent, attenuate, or decrease the rate of onset of any subsequent infection. When provided therapeutically, the agent(s) are provided at (or shortly after) the onset of an indication of infection. The therapeutic administration of the compound(s)

serves to attenuate the pathological symptoms of the infection and to increase the rate of recovery.

The agents of the present invention are administered to a subject, such as a mammal, or a patient, in a pharmaceutically acceptable form and in a therapeutically effective concentration. A composition is said to be "pharmacologically acceptable" if its administration can be tolerated by a recipient patient. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

The agents of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby these materials, or their functional derivatives, are combined in a mixture with a pharmaceutically acceptable carrier vehicle. Suitable vehicles and their formulation, inclusive of other human proteins, *e.g.*, human serum albumin, are described, for example, in REMINGTON'S PHARMACEUTICAL SCIENCES, 16th Ed., Osol, A., Ed., Mack Publishing, Easton PA (1980). In order to form a pharmaceutically acceptable composition suitable for effective administration, such compositions will contain an effective amount of one or more of the agents of the present invention, together with a suitable amount of carrier vehicle.

Additional pharmaceutical methods may be employed to control the duration of action. Control release preparations may be achieved through the use of polymers to complex or absorb one or more of the agents of the present invention. The controlled delivery may be effectuated by a variety of well known techniques, including formulation with macromolecules such as, for example, polyesters, polyamino acids, polyvinyl, pyrrolidone, ethylenevinylacetate, methylcellulose, carboxymethylcellulose, or protamine, sulfate, adjusting the concentration of the macromolecules and the agent in the formulation, and by appropriate use of methods of incorporation, which can be manipulated to effectuate a desired time course of release. Another possible method to control the duration of action by controlled release preparations is to incorporate agents of the present invention into particles of a polymeric material such as polyesters, polyamino acids, hydrogels, poly(lactic acid) or ethylene vinylacetate copolymers. Alternatively, instead of incorporating these agents into polymeric particles, it is possible to entrap these materials in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization with, for example, hydroxymethylcellulose or gelatine-

microcapsules and poly(methylmethacylate) microcapsules, respectively, or in colloidal drug delivery systems, for example, liposomes, albumin microspheres, microemulsions, nanoparticles, and nanocapsules or in macroemulsions. Such techniques are disclosed in REMINGTON'S PHARMACEUTICAL SCIENCES (1980).

The invention further provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

In addition, the agents of the present invention may be employed in conjunction with other therapeutic compounds.

6. Shot-Gun Approach to Megabase DNA Sequencing

The present invention further demonstrates that a large sequence can be sequenced using a random shotgun approach. This procedure, described in detail in the examples that follow, has eliminated the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols.

Certain aspects of the present invention are described in greater detail in the examples that follow. The examples are provided by way of illustration. Other aspects and embodiments of the present invention are contemplated by the inventors, as will be clear to those of skill in the art from reading the present disclosure.

ILLUSTRATIVE EXAMPLES

LIBRARIES AND SEQUENCING

1. Shotgun Sequencing Probability Analysis

The overall strategy for a shotgun approach to whole genome sequencing follows from the Lander and Waterman (Landerman and Waterman, *Genomics* 2:231 (1988)) application of the equation for the Poisson distribution. According to this treatment, the probability, P_0, that any given base in a sequence of size L, in nucleotides, is not sequenced after a certain amount, n, in nucleotides, of random

sequence has been determined can be calculated by the equation $P_0 = e^{-m}$, where m is L/n, the fold coverage. For instance, for a genome of 2.8 Mb, m=1 when 2.8 Mb of sequence has been randomly generated (1X coverage). At that point, $P_0 = e^{-1} = 0.37$. The probability that any given base has not been sequenced is the same as the probability that any region of the whole sequence L has not been determined and, therefore, is equivalent to the fraction of the whole sequence that has yet to be determined. Thus, at one-fold coverage, approximately 37% of a polynucleotide of size L, in nucleotides has not been sequenced. When 14 Mb of sequence has been generated, coverage is 5X for a 2.8 Mb and the unsequenced fraction drops to .0067 or 0.67%. 5X coverage of a 2.8 Mb sequence can be attained by sequencing approximately 17,000 random clones from both insert ends with an average sequence read length of 410 bp.

Similarly, the total gap length, G, is determined by the equation $G = Le^{-m}$, and the average gap size, g, follows the equation, g = L/n. Thus, 5X coverage leaves about 240 gaps averaging about 82 bp in size in a sequence of a polynucleotide 2.8 Mb long.

The treatment above is essentially that of Lander and Waterman, *Genomics* 2: 231 (1988).

2. Random Library Construction

In order to approximate the random model described above during actual sequencing, a nearly ideal library of cloned genomic fragments is required. The following library construction procedure was developed to achieve this end.

Streptococcus pneumoniae DNA is prepared by phenol extraction. A mixture containing 200 µg DNA in 1.0 ml of 300 mM sodium acetate, 10 mM Tris-HCl, 1 mM Na-EDTA, 50% glycerol is processed through a nebulizer (IPI Medical Products) with a stream of nitrogen adjusted to 35 Kpa for 2 minutes. The sonicated DNA is ethanol precipitated and redissolved in 500 µl TE buffer.

To create blunt-ends, a 100 µl aliquot of the resuspended DNA is digested with 5 units of BAL31 nuclease (New England BioLabs) for 10 min at 30°C in 200 µl BAL31 buffer. The digested DNA is phenol-extracted, ethanol-precipitated, redissolved in 100 µl TE buffer, and then size-fractionated by electrophoresis through a 1.0% low melting temperature agarose gel. The section containing DNA fragments 1.6-2.0 kb in size is excised from the gel, and the LGT agarose is melted and the resulting solution is extracted with phenol to separate the agarose from the

DNA. DNA is ethanol precipitated and redissolved in 20 µl of TE buffer for ligation to vector.

A two-step ligation procedure is used to produce a plasmid library with 97% inserts, of which >99% were single inserts. The first ligation mixture (50 ul) contains 2 µg of DNA fragments, 2 µg pUC18 DNA (Pharmacia) cut with SmaI and dephosphorylated with bacterial alkaline phosphatase, and 10 units of T4 ligase (GIBCO/BRL) and is incubated at 14°C for 4 hr. The ligation mixture then is phenol extracted and ethanol precipitated, and the precipitated DNA is dissolved in 20 µl TE buffer and electrophoresed on a 1.0% low melting agarose gel. Discrete bands in a ladder are visualized by ethidium bromide-staining and UV illumination and identified by size as insert (I), vector (v), v+I, v+2i, v+3i, *etc.* The portion of the gel containing v+I DNA is excised and the v+I DNA is recovered and resuspended into 20 µl TE. The v+I DNA then is blunt-ended by T4 polymerase treatment for 5 min. at 37°C in a reaction mixture (50 ul) containing the v+I linears, 500 µM each of the 4 dNTPs, and 9 units of T4 polymerase (New England BioLabs), under recommended buffer conditions. After phenol extraction and ethanol precipitation the repaired v+I linears are dissolved in 20 µl TE. The final ligation to produce circles is carried out in a 50 µl reaction containing 5 µl of v+I linears and 5 units of T4 ligase at 14°C overnight. After 10 min. at 70°C the following day, the reaction mixture is stored at -20°C.

This two-stage procedure results in a molecularly random collection of single-insert plasmid recombinants with minimal contamination from double-insert chimeras (<1%) or free vector (<3%).

Since deviation from randomness can arise from propagation the DNA in the host, *E. coli* host cells deficient in all recombination and restriction functions (A. Greener, *Strategies 3 (1)*:5 (1990)) are used to prevent rearrangements, deletions, and loss of clones by restriction. Furthermore, transformed cells are plated directly on antibiotic diffusion plates to avoid the usual broth recovery phase which allows multiplication and selection of the most rapidly growing cells.

Plating is carried out as follows. A 100 µl aliquot of Epicurian Coli SURE II Supercompetent Cells (Stratagene 200152) is thawed on ice and transferred to a chilled Falcon 2059 tube on ice. A 1.7 µl aliquot of 1.42 M beta-mercaptoethanol is added to the aliquot of cells to a final concentration of 25 mM. Cells are incubated on ice for 10 min. A 1 µl aliquot of the final ligation is added to the cells and incubated on ice for 30 min. The cells are heat pulsed for 30 sec. at 42°C and

placed back on ice for 2 min. The outgrowth period in liquid culture is eliminated from this protocol in order to minimize the preferential growth of any given transformed cell. Instead the transformation mixture is plated directly on a nutrient rich SOB plate containing a 5 ml bottom layer of SOB agar (5% SOB agar: 20 g tryptone, 5 g yeast extract, 0.5 g NaCl, 1.5% Difco Agar per liter of media). The 5 ml bottom layer is supplemented with 0.4 ml of 50 mg/ml ampicillin per 100 ml SOB agar. The 15 ml top layer of SOB agar is supplemented with 1 ml X-Gal (2%), 1 ml $MgCl_2$ (1 M), and 1 ml $MgSO_4$ /100 ml SOB agar. The 15 ml top layer is poured just prior to plating. Our titer is approximately 100 colonies/10 µl aliquot of transformation.

All colonies are picked for template preparation regardless of size. Thus, only clones lost due to "poison" DNA or deleterious gene products are deleted from the library, resulting in a slight increase in gap number over that expected.

3. Random DNA Sequencing

High quality double stranded DNA plasmid templates are prepared using a "boiling bead" method developed in collaboration with Advanced Genetic Technology Corp. (Gaithersburg, MD) (Adams *et al.*, *Science 252*:1651 (1991); Adams *et al.*, *Nature 355:*632 (1992)). Plasmid preparation is performed in a 96-well format for all stages of DNA preparation from bacterial growth through final DNA purification. Template concentration is determined using Hoechst Dye and a Millipore Cytofluor. DNA concentrations are not adjusted, but low-yielding templates are identified where possible and not sequenced.

Templates are also prepared from two *Streptococcus pneumoniae* lambda genomic libraries. An amplified library is constructed in the vector Lambda GEM-12 (Promega) and an unamplified library is constructed in Lambda DASH II (Stratagene). In particular, for the unamplified lambda library, *Streptococcus pneumoniae* DNA (> 100 kb) is partially digested in a reaction mixture (200 ul) containing 50 µg DNA, 1X Sau3AI buffer, 20 units Sau3AI for 6 min. at 23°C. The digested DNA was phenol-extracted and electrophoresed on a 0.5% low melting agarose gel at 2V/cm for 7 hours. Fragments from 15 to 25 kb are excised and recovered in a final volume of 6 ul. One µl of fragments is used with 1 µl of DASHII vector (Stratagene) in the recommended ligation reaction. One µl of the ligation mixture is used per packaging reaction following the recommended protocol with the Gigapack II XL Packaging Extract (Stratagene, #227711). Phage

are plated directly without amplification from the packaging mixture (after dilution with 500 µl of recommended SM buffer and chloroform treatment). Yield is about 2.5×10^3 pfu/ul. The amplified library is prepared essentially as above except the lambda GEM-12 vector is used. After packaging, about 3.5×10^4 pfu are plated on the restrictive NM539 host. The lysate is harvested in 2 ml of SM buffer and stored frozen in 7% dimethylsulfoxide. The phage titer is approximately 1×10^9 pfu/ml.

Liquid lysates (100 µl) are prepared from randomly selected plaques (from the unamplified library) and template is prepared by long-range PCR using T7 and T3 vector-specific primers.

Sequencing reactions are carried out on plasmid and/or PCR templates using the AB Catalyst LabStation with Applied Biosystems PRISM Ready Reaction Dye Primer Cycle Sequencing Kits for the M13 forward (M13-21) and the M13 reverse (M13RP1) primers (Adams *et al.*, *Nature 368*:474 (1994)). Dye terminator sequencing reactions are carried out on the lambda templates on a Perkin-Elmer 9600 Thermocycler using the Applied Biosystems Ready Reaction Dye Terminator Cycle Sequencing kits. T7 and SP6 primers are used to sequence the ends of the inserts from the Lambda GEM-12 library and T7 and T3 primers are used to sequence the ends of the inserts from the Lambda DASH II library. Sequencing reactions are performed by eight individuals using an average of fourteen AB 373 DNA Sequencers per day. All sequencing reactions are analyzed using the Stretch modification of the AB 373, primarily using a 34 cm well-to-read distance. The overall sequencing success rate very approximately is about 85% for M13-21 and M13RP1 sequences and 65% for dye-terminator reactions. The average usable read length is 485 bp for M13-21 sequences, 445bp for M13RP1 sequences, and 375 bp for dye-terminator reactions.

Richards *et al.,* Chapter 28 in AUTOMATED DNA SEQUENCING AND ANALYSIS, M. D. Adams, C. Fields, J. C. Venter, Eds., Academic Press, London, (1994) described the value of using sequence from both ends of sequencing templates to facilitate ordering of contigs in shotgun assembly projects of lambda and cosmid clones. We balance the desirability of both-end sequencing (including the reduced cost of lower total number of templates) against shorter read-lengths for sequencing reactions performed with the M13RP1 (reverse) primer compared to the M13-21 (forward) primer. Approximately one-half of the templates are sequenced from both ends. Random reverse sequencing reactions are

done based on successful forward sequencing reactions. Some M13RP1 sequences are obtained in a semi-directed fashion: M13-21: sequences pointing outward at the ends of contigs are chosen for M13RP1 sequencing in an effort to specifically order contigs.

4. Protocol for Automated Cycle Sequencing

The sequencing is carried out using ABI Catalyst robots and AB 373 Automated DNA Sequencers. The Catalyst robot is a publicly available sophisticated pipetting and temperature control robot which has been developed specifically for DNA sequencing reactions. The Catalyst combines pre-aliquoted templates and reaction mixes consisting of deoxy- and dideoxynucleotides, the thermostable Taq DNA polymerase, fluorescently-labelled sequencing primers, and reaction buffer. Reaction mixes and templates are combined in the wells of an aluminum 96-well thermocycling plate. Thirty consecutive cycles of linear amplification (i.*e*.., one primer synthesis) steps are performed including denaturation, annealing of primer and template, and extension; *i.e.*, DNA synthesis. A heated lid with rubber gaskets on the thermocycling plate prevents evaporation without the need for an oil overlay.

Two sequencing protocols are used: one for dye-labelled primers and a second for dye-labelled dideoxy chain terminators. The shotgun sequencing involves use of four dye-labelled sequencing primers, one for each of the four terminator nucleotide. Each dye-primer is labelled with a different fluorescent dye, permitting the four individual reactions to be combined into one lane of the 373 DNA Sequencer for electrophoresis, detection, and base-calling. ABI currently supplies pre-mixed reaction mixes in bulk packages containing all the necessary non-template reagents for sequencing. Sequencing can be done with both plasmid and PCR- generated templates with both dye-primers and dye- terminators with approximately equal fidelity, although plasmid templates generally give longer usable sequences.

Thirty-two reactions are loaded per AB373 Sequencer each day, for a total of 960 samples. Electrophoresis is run overnight following the manufacturer's protocols, and the data is collected for twelve hours. Following electrophoresis and fluorescence detection, the ABI 373 performs automatic lane tracking and base-calling. The lane-tracking is confirmed visually. Each sequence electropherogram (or fluorescence lane trace) is inspected visually and assessed for quality. Trailing

sequences of low quality are removed and the sequence itself is loaded via software to a Sybase database (archived daily to 8mm tape). Leading vector polylinker sequence is removed automatically by a software program. Average edited lengths of sequences from the standard ABI 373 are around 400 bp and depend mostly on the quality of the template used for the sequencing reaction. ABI 373 Sequencers converted to Stretch Liners provide a longer electrophoresis path prior to fluorescence detection and increase the average number of usable bases to 500-600 bp.

INFORMATICS

1. Data Management

A number of information management systems for a large-scale sequencing lab have been developed. (For review see, for instance, Kerlavage *et al.*, *Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences*, IEEE Computer Society Press, Washington D. C., 585 (1993)) The system used to collect and assemble the sequence data was developed using the Sybase relational database management system and was designed to automate data flow wherever possible and to reduce user error. The database stores and correlates all information collected during the entire operation from template preparation to final analysis of the genome. Because the raw output of the ABI 373 Sequencers was based on a Macintosh platform and the data management system chosen was based on a Unix platform, it was necessary to design and implement a variety of multi- user, client-server applications which allow the raw data as well as analysis results to flow seamlessly into the database with a minimum of user effort.

2. Assembly

An assembly engine (TIGR Assembler) developed for the rapid and accurate assembly of thousands of sequence fragments was employed to generate contigs. The TIGR assembler simultaneously clusters and assembles fragments of the genome. In order to obtain the speed necessary to assemble more than 10^4 fragments, the algorithm builds a hash table of 12 bp oligonucleotide subsequences to generate a list of potential sequence fragment overlaps. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Beginning with a single seed sequence fragment, TIGR Assembler extends the current contig by attempting to add the best matching

fragment based on oligonucleotide content. The contig and candidate fragment are aligned using a modified version of the Smith-Waterman algorithm which provides for optimal gapped alignments (Waterman, M. S., *Methods in Enzymology 164*:765 (1988)). The contig is extended by the fragment only if strict criteria for the quality of the match are met. The match criteria include the minimum length of overlap, the maximum length of an unmatched end, and the minimum percentage match. These criteria are automatically lowered by the algorithm in regions of minimal coverage and raised in regions with a possible repetitive element. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Fragments representing the boundaries of repetitive elements and potentially chimeric fragments are often rejected based on partial mismatches at the ends of alignments and excluded from the current contig. TIGR Assembler is designed to take advantage of clone size information coupled with sequencing from both ends of each template. It enforces the constraint that sequence fragments from two ends of the same template point toward one another in the contig and are located within a certain range of base pairs (definable for each clone based on the known clone size range for a given library).

The process resulted in 391 contigs as represented by SEQ ID NOs:1-391.

3. Identifying Genes

The predicted coding regions of the *Streptococcus pneumoniae* genome were initially defined with the program GeneMark, which finds ORFs using a probabilistic classification technique. The predicted coding region sequences were used in searches against a database of all nucleotide sequences from GenBank (October, 1997), using the BLASTN search method to identify overlaps of 50 or more nucleotides with at least a 95% identity. Those ORFs with nucleotide sequence matches are shown in Table 1. The ORFs without such matches were translated to protein sequences and compared to a non-redundant database of known proteins generated by combining the Swiss-prot, PIR and GenPept databases. ORFs that matched a database protein with BLASTP probability less than or equal to 0.01 are shown in Table 2. The table also lists assigned functions based on the closest match in the databases. ORFs that did not match protein or nucleotide sequences in the databases at these levels are shown in Table 3.

ILLUSTRATIVE APPLICATIONS

1. Production of an Antibody to a *Streptococcus pneumoniae* Protein

Substantially pure protein or polypeptide is isolated from the transfected or transformed cells using any one of the methods known in the art. The protein can also be produced in a recombinant prokaryotic expression system, such as *E. coli*, or can be chemically synthesized. Concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows.

2. Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., *Nature 256*:495 (1975) or modifications of the methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, E., *Meth. Enzymol. 70:*419 (1980), and modified methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. *et al.*, *Basic Methods in Molecular Biology,* Elsevier, New York. Section 21-2 (1989).

3. Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than others and may require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. *et al.*, *J. Clin.* Endocrinol. Metab. 33:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, O. *et al.*, Chap. 19 in: *Handbook of Experimental Immunology,* Wier, D., ed, Blackwell (1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, second edition, Rose and Friedman, eds., Amer. Soc. For Microbiology, Washington, D. C. (1980)

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi- quantitatively or qualitatively to identify the presence of antigen in a biological sample. In addition, antibodies are useful in various animal models of pneumococcal disease as a means of evaluating the protein used to make the antibody as a potential vaccine target or as a means of evaluating the antibody as a potential immunotherapeutic or immunoprophylactic reagent.

4. Preparation of PCR Primers and Amplification of DNA

Various fragments of the *Streptococcus pneumoniae* genome, such as those of Tables 1-3 and SEQ ID NOS:1-391 can be used, in accordance with the present invention, to prepare PCR primers for a variety of uses. The PCR primers are preferably at least 15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. The PCR primers and amplified DNA of this Example find use in the Examples that follow.

5. Gene expression from DNA Sequences Corresponding to ORFs

A fragment of the *Streptococcus pneumoniae* genome provided in Tables 1-3 is introduced into an expression vector using conventional technology. Techniques to transfer cloned sequences into expression vectors that direct protein translation in mammalian, yeast, insect or bacterial expression systems are well known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism, as explained by Hatfield *et al.*, U. S. Patent No. 5,082,767, incorporated herein by this reference.

The following is provided as one exemplary method to generate polypeptide(s) from cloned ORFs of the *Streptococcus pneumoniae* genome fragment. Bacterial ORFs generally lack a poly A addition signal. The addition signal sequence can be added to the construct by, for example, splicing out the poly A addition sequence from pSG5 (Stratagene) using BglI and SalI restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene) for use in eukaryotic expression systems. pXT1 contains the LTRs and a portion of the gag gene of Moloney Murine Leukemia Virus. The positions of the LTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex thymidine kinase promoter and the selectable neomycin gene. The *Streptococcus pneumoniae* DNA is obtained by PCR from the bacterial vector using oligonucleotide primers complementary to the *Streptococcus pneumoniae* DNA and containing restriction endonuclease sequences for PstI incorporated into the 5' primer and BglII at the 5' end of the corresponding *Streptococcus pneumoniae* DNA 3' primer, taking care to ensure that the *Streptococcus pneumoniae* DNA is positioned such that its followed with the poly A addition sequence. The purified fragment obtained from the resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with BglII, purified and ligated to pXT1, now containing a poly A addition sequence and digested BglII.

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600 ug/ml G418 (Sigma, St. Louis, Missouri). The protein is preferably released into the supernatant. However if the protein has membrane binding domains, the protein may additionally be retained within the cell or expression may be restricted to the cell surface. Since it may be necessary to purify and locate the transfected product, synthetic 15-mer peptides synthesized from the predicted *Streptococcus pneumoniae* DNA sequence are injected into mice to generate antibody to the polypeptide encoded by the *Streptococcus pneumoniae* DNA.

Alternatively and if antibody production is not possible, the *Streptococcus pneumoniae* DNA sequence is additionally incorporated into eukaryotic expression vectors and expressed as, for example, a globin fusion. Antibody to the globin moiety then is used to purify the chimeric protein. Corresponding protease cleavage sites are engineered between the globin moiety and the polypeptide encoded by the *Streptococcus pneumoniae* DNA so that the latter may be freed from the formed by simple protease digestion. One useful expression vector for generating globin chimerics is pSG5 (Stratagene). This vector encodes a rabbit globin. Intron II of the rabbit globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques are well known to those skilled in the art of molecular biology. Standard methods are published in methods texts such as Davis *et al.*, cited elsewhere herein, and many of the methods are available from the technical assistance representatives from Stratagene, Life Technologies, Inc., or Promega. Polypeptides of the invention also may be produced using *in vitro* translation systems such as *in vitro* ExpressTM Translation Kit (Stratagene).

While the present invention has been described in some detail for purposes of clarity and understanding, one skilled in the art will appreciate that various changes in form and detail can be made without departing from the true scope of the invention.

All patents, patent applications and publications referred to above are hereby incorporated by reference.

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
1	1	437	1003	gb|U41735|	Streptococcus pneumoniae peptide methionine sulfoxide reductase (msrA) and homoserine kinase homolog (thrB) genes, complete cds	92	200	567
2	5	6169	5720	gb|U04047|	Streptococcus pneumoniae SSZ dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	96	450	450
2	6	6592	6167	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	98	426	426
3	11	9770	9147	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	94	624	624
3	12	10489	9671	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	91	819	819
3	13	11546	12019	gb|U43526|	Streptococcus pneumoniae neuraminidase B (nanB) gene, complete cds, and neuraminidase (nanA) gene, partial cds	99	474	474
3	14	12017	13375	gb|U43526|	Streptococcus pneumoniae neuraminidase B (nanB) gene, complete cds, and neuraminidase (nanA) gene, partial cds	99	1359	1359
3	15	13421	14338	gb|U43526|	Streptococcus pneumoniae neuraminidase B (nanB) gene, complete cds, and neuraminidase (nanA) gene, partial cds	99	918	918
3	16	14329	15171	gb|U43526|	Streptococcus pneumoniae neuraminidase B (nanB) gene, complete cds, and neuraminidase (nanA) gene, partial cds	99	843	843
3	17	15132	17282	gb|U43526|	Streptococcus pneumoniae neuraminidase B (nanB) gene, complete cds, and neuraminidase (nanA) gene, partial cds	99	2151	2151
3	18	17267	18397	gb|U43526|	Streptococcus pneumoniae neuraminidase B (nanB) gene, complete cds, and neuraminidase (nanA) gene, partial cds	99	1069	1131
4	1	46	1188	emb|Y11463|SPDN	Streptococcus pneumoniae dnaG, rpoD, cpoA genes and ORF3 and ORF5	99	1143	1143
4	2	1198	2529	emb|Y11463|SPDN	Streptococcus pneumoniae dnaG, rpoD, cpoA genes and ORF3 and ORF5	99	876	1332
5	7	11297	11473	gb|U41735|	Streptococcus pneumoniae peptide methionine sulfoxide reductase (msrA) and homoserine kinase homolog (thrB) genes, complete cds	82	175	177
6	7	7125	7364	emb|Z77726|SPIS	S.pneumoniae DNA for insertion sequence IS1318 (1372 bp)	93	238	240
6	8	7322	7570	emb|Z77725|SPIS	S.pneumoniae DNA for insertion sequence IS1381 (966 bp)	95	160	249
6	9	7533	7985	emb|Z77725|SPIS	S.pneumoniae DNA for insertion sequence IS1381 (966 bp)	99	453	453
6	23	20197	19733	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	96	465	465
7	10	8305	7682	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	95	624	624

TABLE 1

S. pneumoniae - Coding regions containing known sequences

<table>
<tr><th>Contig ID</th><th>ORF ID</th><th>Start (nt)</th><th>Stop (nt)</th><th>match acession</th><th>match gene name</th><th>percent ident</th><th>HSP nt length</th><th>ORF nt length</th></tr>
<tr><td>7</td><td>11</td><td>9024</td><td>8206</td><td>emb|Z83335|SPZ8</td><td>S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene</td><td>95</td><td>819</td><td>819</td></tr>
<tr><td>10</td><td>13</td><td>9304</td><td>8078</td><td>gb|L29323|</td><td>Streptococcus pneumoniae methyl transferase (mtr) gene cluster, complete cds</td><td>93</td><td>513</td><td>1227</td></tr>
<tr><td>11</td><td>2</td><td>548</td><td>919</td><td>emb|Z79691|SOOR</td><td>S.pneumoniae yorf[A,B,C,D,E], ftsL, pbpX and regR genes</td><td>99</td><td>316</td><td>372</td></tr>
<tr><td>11</td><td>3</td><td>892</td><td>1980</td><td>emb|Z79691|SOOR</td><td>S.pneumoniae yorf[A,B,C,D,E], ftsL, pbpX and regR genes</td><td>99</td><td>1089</td><td>1089</td></tr>
<tr><td>11</td><td>5</td><td>3040</td><td>3477</td><td>emb|Z79691|SOOR</td><td>S.pneumoniae yorf[A,B,C,D,E], ftsL, pbpX and regR genes</td><td>99</td><td>259</td><td>438</td></tr>
<tr><td>11</td><td>6</td><td>3480</td><td>3247</td><td>emb|Z79691|SOOR</td><td>S.pneumoniae yorf[A,B,C,D,E], ftsL, pbpX and regR genes</td><td>99</td><td>234</td><td>234</td></tr>
<tr><td>11</td><td>7</td><td>3601</td><td>4557</td><td>emb|Z79691|SOOR</td><td>S.pneumoniae yorf[A,B,C,D,E], ftsL, pbpX and regR genes</td><td>98</td><td>957</td><td>957</td></tr>
<tr><td>11</td><td>8</td><td>4506</td><td>4886</td><td>emb|Z79691|SOOR</td><td>S.pneumoniae yorf[A,B,C,D,E], ftsL, pbpX and regR genes</td><td>99</td><td>381</td><td>381</td></tr>
<tr><td>11</td><td>9</td><td>4884</td><td>7142</td><td>emb|X16367|SPPB</td><td>Streptococcus pneumoniae pbpX gene for penicillin binding protein 2X</td><td>99</td><td>2259</td><td>2259</td></tr>
<tr><td>11</td><td>10</td><td>7132</td><td>8124</td><td>emb|X16367|SPPB</td><td>Streptococcus pneumoniae pbpX gene for penicillin binding protein 2X</td><td>98</td><td>70</td><td>993</td></tr>
<tr><td>13</td><td>1</td><td>53</td><td>1126</td><td>gb|M31296|</td><td>S.pneumoniae recP gene, complete cds</td><td>99</td><td>437</td><td>1074</td></tr>
<tr><td>14</td><td>3</td><td>1837</td><td>2148</td><td>emb|Z83335|SPZ8</td><td>S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene</td><td>87</td><td>96</td><td>312</td></tr>
<tr><td>14</td><td>4</td><td>2518</td><td>2108</td><td>gb|M36180|</td><td>Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds</td><td>98</td><td>411</td><td>411</td></tr>
<tr><td>15</td><td>9</td><td>8942</td><td>8511</td><td>gb|U09239|</td><td>Streptococcus pneumoniae type 19F capsular polysaccharide biosynthesis operon, (cps19fABCDEFGHIJKLMNO) genes, complete cds, and aliA gene, partial cds</td><td>89</td><td>340</td><td>432</td></tr>
<tr><td>17</td><td>7</td><td>3910</td><td>3458</td><td>emb|Z77726|SPIS</td><td>S.pneumoniae DNA for insertion sequence IS1318 (1372 bp)</td><td>98</td><td>453</td><td>453</td></tr>
<tr><td>17</td><td>8</td><td>4304</td><td>3873</td><td>emb|Z77727|SPIS</td><td>S.pneumoniae DNA for insertion sequence IS1318 (823 bp)</td><td>96</td><td>382</td><td>432</td></tr>
<tr><td>19</td><td>1</td><td>41</td><td>529</td><td>emb|X94909|SPIG</td><td>S.pneumoniae iga gene</td><td>75</td><td>368</td><td>489</td></tr>
<tr><td>19</td><td>2</td><td>554</td><td>757</td><td>gb|L07752|</td><td>Streptococcus pneumoniae attachment site (attB), DNA sequence</td><td>99</td><td>167</td><td>204</td></tr>
<tr><td>19</td><td>3</td><td>946</td><td>1827</td><td>gb|L07752|</td><td>Streptococcus pneumoniae attachment site (attB), DNA sequence</td><td>94</td><td>100</td><td>882</td></tr>
<tr><td>20</td><td>1</td><td>937</td><td>182</td><td>gb|U33315|</td><td>Streptococcus pneumoniae orfL gene, partial cds, competence stimulating peptide precursor (comC), histidine protein kinase (comD) and response regulator (comE) genes, complete cds, tRNA-Arg and tRNA-Gln genes</td><td>99</td><td>756</td><td>756</td></tr>
<tr><td>20</td><td>2</td><td>2271</td><td>931</td><td>gb|U33315|</td><td>Streptococcus pneumoniae orfL gene, partial cds, competence stimulating peptide precursor (comC), histidine protein kinase (comD) and response regulator (comE) genes, complete cds, tRNA-Arg and tRNA-Gln genes</td><td>98</td><td>1341</td><td>1341</td></tr>
</table>

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
20	3	3175	2684	gb|U76218|	Streptococcus pneumoniae competence stimulating peptide precursor ComC (comC), histidine kinase homolog ComD (comD), and response regulator homolog ComE (comE) genes, complete cds	99	492	492
20	4	3322	4527	gb|AF000658|	Streptococcus pneumoniae R801 tRNA-Arg gene, partial sequence, and putative serine protease (sphtra), SPSpoJ (spspoJ), initiator protein (spdnaa) and beta subunit of DNA polymerase III (spdnan) genes, complete cds	99	1206	1206
20	5	4573	5343	gb|AF000658|	Streptococcus pneumoniae R801 tRNA-Arg gene, partial sequence, and putative serine protease (sphtra), SPSpoJ (spspoJ), initiator protein (spdnaa) and beta subunit of DNA polymerase III (spdnan) genes, complete cds	99	771	771
20	6	5532	6917	gb|AF000658|	Streptococcus pneumoniae R801 tRNA-Arg gene, partial sequence, and putative serine protease (sphtra), SPSpoJ (spspoJ), initiator protein (spdnaa) and beta subunit of DNA polymerase III (spdnan) genes, complete cds	99	1386	1386
20	7	6995	8212	gb|AF000658|	Streptococcus pneumoniae R801 tRNA-Arg gene, partial sequence, and putative serine protease (sphtra), SPSpoJ (spspoJ), initiator protein (spdnaa) and beta subunit of DNA polymerase III (spdnan) genes, complete cds	99	1218	1218
20	8	8214	8471	gb|AF000658|	Streptococcus pneumoniae R801 tRNA-Arg gene, partial sequence, and putative serine protease (sphtra), SPSpoJ (spspoJ), initiator protein (spdnaa) and beta subunit of DNA polymerase III (spdnan) genes, complete cds	98	258	258
20	9	8534	9670	gb|AF000658|	Streptococcus pneumoniae R801 tRNA-Arg gene, partial sequence, and putative serine protease (sphtra), SPSpoJ (spspoJ), initiator protein (spdnaa) and beta subunit of DNA polymerase III (spdnan) genes, complete cds	99	134	1137
22	14	11887	12267	emb|Z77726|SPIS	S.pneumoniae DNA for insertion sequence IS1318 (1372 bp)	99	226	381
22	15	12708	12256	emb|Z77727|SPIS	S.pneumoniae DNA for insertion sequence IS1318 (823 bp)	97	353	453
22	16	13165	12662	emb|Z77726|SPIS	S.pneumoniae DNA for insertion sequence IS1318 (1372 bp)	98	504	504
22	23	18398	18910	emb|Z86112|SPZ8	S.pneumoniae genes encoding galacturonosyl transferase and transposase and insertion sequence IS1515	95	463	513
22	24	18829	19299	emb|Z86112|SPZ8	S.pneumoniae genes encoding galacturonosyl transferase and transposase and insertion sequence IS1515	99	443	471
23	5	5624	4203	emb|X52474|SPPL	S.pneumoniae ply gene for pneumolysin	99	1422	1422
23	6	6063	5629	gb|M17717|	S.pneumoniae pneumolysin gene, complete cds	98	197	435
26	1	5500	2	emb|X94909|SPIG	S.pneumoniae iga gene	87	3487	5499
26	2	5823	5584	gb|U47687|	Streptococcus pneumoniae immunoglobulin A1 protease (iga) gene, complete cds	99	151	240
26	3	6878	5685	gb|U47687|	Streptococcus pneumoniae immunoglobulin A1 protease (iga) gene, complete cds	100	50	1194

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
26	8	14498	14854	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	99	338	357
26	9	14763	14924	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	100	94	162
26	10	14922	15173	gb|U04047|	Streptococcus pneumoniae SSZ dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	97	242	252
28	1	80	505	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	99	426	426
28	2	503	952	gb|U04047|	Streptococcus pneumoniae SSZ dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	97	450	450
28	3	780	1298	gb|U04047|	Streptococcus pneumoniae SSZ dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	96	181	519
34	1	207	1523	gb|L08611|	Streptococcus pneumoniae maltose/maltodextrin uptake (malX) and two maltodextrin permease (malC and malD) genes, complete cds	99	1317	1317
34	2	1477	2367	gb|L08611|	Streptococcus pneumoniae maltose/maltodextrin uptake (malX) and two maltodextrin permease (malC and malD) genes, complete cds	96	795	891
34	3	2593	3420	gb|L21856|	Streptococcus pneumoniae malA gene, complete cds; malR gene, complete cds	96	446	828
34	4	2790	2647	gb|L21856|	Streptococcus pneumoniae malA gene, complete cds; malR gene, complete cds	98	137	144
34	5	3418	4416	gb|L21856|	Streptococcus pneumoniae malA gene, complete cds; malR gene, complete cds	96	999	999
34	9	7764	7507	gb|U41735|	Streptococcus pneumoniae peptide methionine sulfoxide reductase (msrA) and homoserine kinase homolog (thrB) genes, complete cds	93	201	258
34	16	10562	10257	emb|X63602|SPBO	S.pneumoniae mmsA-Box	92	238	306
35	4	1176	1439	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	87	248	264
35	5	1458	1961	gb|U09239|	Streptococcus pneumoniae type 19F capsular polysaccharide biosynthesis operon, (cps19fABCDEFGHIJKLMNO) genes, complete cds, and aliA gene, partial cds	98	264	504
35	17	16172	15477	emb|X85787|SPCP	S.pneumoniae dexB, cps14A, cps14B, cps14C, cps14D, cps14E, cps14F, cps14G, cps14H, cps14I, cps14J, cps14K, cps14L, tasA genes	97	696	696
35	18	16961	16170	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	86	792	792
35	19	17620	16871	gb|U09239|	Streptococcus pneumoniae type 19F capsular polysaccharide biosynthesis operon, (cps19fABCDEFGHIJKLMNO) genes, complete cds, and aliA gene, partial cds	83	750	750

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
35	20	19061	17604	emb|X85787|SPCP	S.pneumoniae dexB, cps14A, cps14B, cps14C, cps14D, cps14E, cps14F, cps14G, cps14H, cps14I, cps14J, cps14K, cps14L, tasA genes	94	1458	1458
36	19	18960	18352	gb|U40786|	Streptococcus pneumoniae surface antigen A variant precursor (psaA) and 18 kDa protein genes, complete cds, and ORF1 gene, partial cds	99	609	609
36	20	19934	18966	gb|U53509|	Streptococcus pneumoniae surface adhesin A precursor (psaA) gene, complete cds	99	969	969
37	1	2743	179	emb|Z67739|SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	99	2565	2565
37	2	2985	2824	emb|Z67739|SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	100	162	162
37	3	5034	3070	emb|Z67739|SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	99	1965	1965
37	4	'5134	5790	emb|Z67739|SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	99	657	657
37	5	6171	5833	emb|Z67739|SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	96	339	339
38	19	12969	13268	gb|M28679|	S.pneumoniae promoter region DNA	100	64	300
39	2	1256	2137	gb|U41735|	Streptococcus pneumoniae peptide methionine sulfoxide reductase (msrA) and homoserine kinase homolog (thrB) genes, complete cds	99	882	882
39	3	2405	3370	gb|U41735|	Streptococcus pneumoniae peptide methionine sulfoxide reductase (msrA) and homoserine kinase homolog (thrB) genes, complete cds	99	966	966
40	9	5253	7208	gb|M29686|	S.pneumoniae mismatch repair (hexB) gene, complete cds	99	1956	1956
41	1	3	1037	emb|Z17307|SPRE	S.pneumoniae recA gene encoding RecA	99	1027	1035
41	2	1328	2713	emb|Z34303|SPCI	Streptococcus pneumoniae cin operon encoding the cinA, recA, dinF, lytA genes, and downstream sequences	99	1386	1386
41	3	3083	4045	gb|M13812|	S.pneumoniae autolysin (lytA) gene, complete cds	99	963	963
41	4	3272	3096	gb|M13812|	S.pneumoniae autolysin (lytA) gene, complete cds	100	177	177
41	5	3603	3860	gb|M13812|	S.pneumoniae autolysin (lytA) gene, complete cds	100	258	258
41	6	4755	5162	gb|L36660|	Streptococcus pneumoniae ORF, complete cds	98	408	408
41	7	5270	5716	gb|L36660|	Streptococcus pneumoniae ORF, complete cds	98	447	447
41	8	6112	6918	gb|L36660|	Streptococcus pneumoniae ORF, complete cds	98	431	807
41	9	6916	7119	gb|L36660|	Streptococcus pneumoniae ORF, complete cds	100	204	204
41	10	7082	7660	gb|L36660|	Streptococcus pneumoniae ORF, complete cds	97	552	579
41	11	7680	7979	gb|L36660|	Streptococcus pneumoniae ORF, complete cds	98	81	300
41	12	9169	8717	emb|Z77727|SPIS	S.pneumoniae DNA for insertion sequence IS1318 (823 bp)	97	353	453

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
41	13	9533	9132	emb|Z77725|SPIS	S.pneumoniae DNA for insertion sequence IS1381 (966 bp)	95	160	402
41	14	9669	9475	emb|Z82001|SPZ8	S.pneumoniae pcpA gene and open reading frames	100	189	195
44	5	7190	7555	emb|Z82001|SPZ8	S.pneumoniae pcpA gene and open reading frames	99	366	366
44	6	8059	7607	emb|Z77726|SPIS	S.pneumoniae DNA for insertion sequence IS1318 (1372 bp)	97	453	453
44	7	8423	8022	emb|Z77725|SPIS	S.pneumoniae DNA for insertion sequence IS1381 (966 bp)	95	160	402
44	8	8559	8365	emb|Z82001|SPZ8	S.pneumoniae pcpA gene and open reading frames	100	189	195
48	9	6480	4687	gb|L39074|	Streptococcus pneumoniae pyruvate oxidase (spxB) gene, complete cds	99	1794	1794
49	2	231	2603	gb|L20561|	Streptococcus pneumoniae Exp7 gene, partial cds	100	216	2373
53	6	2407	2156	gb|U04047|	Streptococcus pneumoniae SSZ dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	97	242	252
53	7	2566	2405	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	100	94	162
53	8	2831	2475	emb|Z83335|SPZ8	S.pneumoniae dexB; cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	99	338	357
54	13	12409	11105	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	67	591	1305
55	22	20488	19949	emb|Z84379|HSZ8	S.pneumoniae dfr gene (isolate 92)	99	540	540
61	11	11864	9900	emb|Z16082|PNAL	Streptococcus pneumoniae aliB gene	98	1965	1965
63	1	3	239	gb|M18729|	S.pneumoniae mismatch repair protein (hexA) gene, complete cds	100	237	237
63	2	233	2611	gb|M18729|	S.pneumoniae mismatch repair protein (hexA) gene, complete cds	99	2330	2379
63	3	2557	2823	gb|M18729|	S.pneumoniae mismatch repair protein (hexA) gene, complete cds	99	266	267
63	4	2958	4664	gb|M18729|	S.pneumoniae mismatch repair protein (hexA) gene, complete cds	95	69	1707
67	6	3770	3399	gb|L20670|	Streptococcus pneumoniae hyaluronidase gene, complete cds	96	372	372
67	7	7161	4171	gb|L20670|	Streptococcus pneumoniae hyaluronidase gene, complete cds	99	2938	2991
70	1	1	702	gb|M14340|	S.pneumoniae DpnI gene region encoding dpnC and dpnD, complete cds	100	693	702
70	2	678	1160	gb|M14340|	S.pneumoniae DpnI gene region encoding dpnC and dpnD, complete cds	100	483	483
70	3	2490	1210	gb|M14339|	S.pneumoniae DpnII gene region encoding dpnM, dpnA, dpnB, complete cds	98	462	1281
70	7	4230	4424	gb|J04234|	S.pneumoniae exodeoxyribonuclease (exoA) gene, complete cds	99	147	195
70	8	5197	4316	gb|J04234|	S.pneumoniae exodeoxyribonuclease (exoA) gene, complete cds	99	881	882

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
70	13	8108	9874	gb|L20562|	Streptococcus pneumoniae Exp8 gene, partial cds	93	234	1767
71	22	27964	28341	emb|X63602|SPBO	S.pneumoniae mmsA-Box	93	233	378
72	5	4607	3552	emb|Z26850|SPAT	S.pneumoniae (M222) genes for ATPase a subunit, ATPase b subunit and ATPase c subunit	97	102	1056
73	1	471	133	emb|X63602|SPBO	S.pneumoniae mmsA-Box	91	193	339
73	3	3658	977	gb|J04479|	S.pneumoniae DNA polymerase I (polA) gene, complete cds	99	2682	2682
73	8	4864	5379	gb|M36180|	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	98	318	516
77	3	2622	1999	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	95	624	624
77	4	3341	2523	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	91	819	819
78	1	341	3	emb|X77249|SPR6	S.pneumoniae (R6) ciaR/ciaH genes	99	339	339
78	2	1095	325	emb|X77249|SPR6	S.pneumoniae (R6) ciaR/ciaH genes	99	771	771
82	10	11436	10816	gb|U90721|	Streptococcus pneumoniae signal peptidase I (spi) gene, complete cds	97	621	621
82	11	12402	11434	gb|U93576|	Streptococcus pneumoniae ribonuclease HII (rnhB) gene, complete cds	98	953	969
82	12	12381	12704	gb|U93576|	Streptococcus pneumoniae ribonuclease HII (rnhB) gene, complete cds	100	51	324
83	8	3212	3550	emb|Z77727|SPIS	S.pneumoniae DNA for insertion sequence IS1318 (823 bp)	97	290	339
83	10	4662	6851	gb|M36180|	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	99	2190	2190
83	11	6849	8213	gb|M36180|	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	99	1365	1365
83	12	8236	9090	gb|M36180|	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	99	855	855
83	13	9283	13017	gb|L15190|	Streptococcus pneumoniae SAICAR synthetase (purC) gene, complete cds	100	107	3735
83	23	22147	23313	gb|L36923|	Streptococcus pneumoniae beta-N-acetylhexosaminidase (strH) gene, complete cds	98	218	1167
83	24	23268	23450	gb|L36923|	Streptococcus pneumoniae beta-N-acetylhexosaminidase (strH) gene, complete cds	98	172	183
83	25	27527	23505	gb|L36923|	Streptococcus pneumoniae beta-N-acetylhexosaminidase (strH) gene, complete cds	99	3826	4023

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
83	26	28472	27771	gb|L36923|	Streptococcus pneumoniae beta-N-acetylhexosaminidase (strH) gene, complete cds	99	416	702
84	4	4554	6173	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	98	697	1620
87	6	5951	5316	emb|Z77725|SPIS	S.pneumoniae DNA for insertion sequence IS1381 (966 bp)	96	439	636
88	5	2957	3511	gb|M36180|	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	94	555	555
88	6	3466	4269	gb|M36180|	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	94	804	804
89	13	9878	10093	gb|M36180|	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	97	211	216
89	14	10062	10412	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	97	335	351
93	10	5303	4941	emb|X63602|SPBO	S.pneumoniae mmsA-Box	89	237	363
97	4	1708	1520	gb|U41735|	Streptococcus pneumoniae peptide methionine sulfoxide reductase (msrA) and homoserine kinase homolog (thrB) genes, complete cds	91	140	189
99	1	89	700	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	93	592	612
99	2	1773	775	emb|X17337|SPAM	Streptococcus pneumoniae ami locus conferring aminopterin resistance	99	998	999
99	3	2794	1712	emb|X17337|SPAM	Streptococcus pneumoniae ami locus conferring aminopterin resistance	99	1083	1083
99	4	3732	2788	emb|X17337|SPAM	Streptococcus pneumoniae ami locus conferring aminopterin resistance	100	945	945
99	5	5249	3714	emb|X17337|SPAM	Streptococcus pneumoniae ami locus conferring aminopterin resistance	100	1536	1536
99	6	7262	5277	emb|X17337|SPAM	Streptococcus pneumoniae ami locus conferring aminopterin resistance	99	1986	1986
101	1	216	1538	emb|X54225|SPEN	S.pneumoniae epuA and endA genes for 7 kDa protein and membrane endonuclease	99	146	1323
101	2	1492	1719	emb|X54225|SPEN	S.pneumoniae epuA and endA genes for 7 kDa protein and membrane endonuclease	99	228	228
101	3	1694	1855	emb|X54225|SPEN	S.pneumoniae epuA and endA genes for 7 kDa protein and membrane endonuclease	100	162	162
101	4	1701	2582	emb|X54225|SPEN	S.pneumoniae epuA and endA genes for 7 kDa protein and membrane endonuclease	100	882	882
103	7	5556	5041	emb|Z95914|SPZ9	Streptococcus pneumoniae sodA gene	100	396	516
104	2	1347	1556	emb|Z77727|SPIS	S.pneumoniae DNA for insertion sequence IS1318 (823 bp)	83	206	210

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
105	5	5381	5028	emb|Z67739|SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	98	353	354
105	6	6089	5379	emb|Z67739|SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	98	84	711
107	4	2785	1880	emb|X16022|SPPE	S.pneumoniae penA gene	98	72	906
107	5	2913	4988	emb|X16022|SPPE	S.pneumoniae penA gene	99	1692	2076
107	6	4981	5595	emb|X13136|SPPE	Streptococcus pneumoniae penA gene for penicillin binding protein 2B lacking N-term. (penicillin resistant strain)	91	107	615
108	9	9068	8718	emb|Z67739|SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	95	342	351
108	12	11308	10922	emb|Z67739|SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	99	199	387
109	3	2768	2241	emb|Z77725|SPIS	S.pneumoniae DNA for insertion sequence IS1381 (966 bp)	96	61	528
109	4	2688	2855	emb|Z77726|SPIS	S.pneumoniae DNA for insertion sequence IS1318 (1372 bp)	96	148	168
109	5	2862	3269	emb|Z77727|SPIS	S.pneumoniae DNA for insertion sequence IS1318 (823 bp)	97	353	408
109	6	5320	3584	gb|M18729|	S.pneumoniae mismatch repair protein (hexA) gene, complete cds	100	371	1737
113	1	431	3	gb|M36180|	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	95	429	429
113	10	9788	8532	emb|X99400|SPDA	S.pneumoniae dacA gene and ORF	99	1257	1257
113	11	9870	10985	emb|X99400|SPDA	S.pneumoniae dacA gene and ORF	99	1116	1116
114	3	2530	2030	gb|M36180|	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	95	481	501
115	11	11303	10932	gb|U04047|	Streptococcus pneumoniae SSZ dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	97	372	372
117	1	897	3302	emb|X72967|SPNA	S.pneumoniae nanA gene	99	2402	2406
117	2	3277	3831	emb|X72967|SPNA	S.pneumoniae nanA gene	99	237	555
117	3	4327	3899	gb|M36180|	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	98	429	429
121	2	1369	1941	gb|U72720|	Streptococcus pneumoniae heat shock protein 70 (dnaK) gene, complete cds and DnaJ (dnaJ) gene, partial cds	99	202	573
121	3	2412	4253	gb|U72720|	Streptococcus pneumoniae heat shock protein 70 (dnaK) gene, complete cds and DnaJ (dnaJ) gene, partial cds	99	1842	1842
122	8	5066	5587	gb|U04047|	Streptococcus pneumoniae SSZ dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	64	451	522

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
125	1	1811	189	gb|M36180|	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	92	99	1623
128	15	12496	11204	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	91	705	1293
134	1	1	492	emb|Y10818|SPY1	S.pneumoniae spsA gene	99	203	492
134	2	556	2652	gb|AF019904|	Streptococcus pneumoniae choline binding protein A (cbpA) gene, partial cds	86	685	2097
134	3	1160	837	emb|Y10818|SPY1	S.pneumoniae spsA gene	86	324	324
134	4	3952	2882	gb|AF019904|	Streptococcus pneumoniae choline binding protein A (cbpA) gene, partial cds	98	215	1071
134	8	7992	9848	gb|U12567|	Streptococcus pneumoniae P13 glycerol-3-phosphate dehydrogenase (glpD) gene, partial cds, and glycerol uptake facilitator (glpF) and ORF3 genes, complete cds	99	285	1857
134	9	9846	10622	gb|U12567|	Streptococcus pneumoniae P13 glycerol-3-phosphate dehydrogenase (glpD) gene, partial cds, and glycerol uptake facilitator (glpF) and ORF3 genes, complete cds	99	570	777
134	10	10805	11122	gb|U12567|	Streptococcus pneumoniae P13 glycerol-3-phosphate dehydrogenase (glpD) gene, partial cds, and glycerol uptake facilitator (glpF) and ORF3 genes, complete cds	100	318	318
137	13	7970	8443	gb|U09239|	Streptococcus pneumoniae type 19F capsular polysaccharide biosynthesis operon, (cps19fABCDEFGHIJKLMNO) genes, complete cds, and aliA gene, partial cds	90	420	474
137	14	8590	8775	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	94	174	186
137	15	8773	8967	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	98	195	195
137	16	9223	9687	emb|Z77726|SPIS	S.pneumoniae DNA for insertion sequence IS1318 (1372 bp)	96	446	465
137	17	9641	10051	emb|Z77727|SPIS	S.pneumoniae DNA for insertion sequence IS1318 (823 bp)	96	293	411
139	10	12998	12702	emb|X63602|SPBO	S.pneumoniae mmsA-Box	90	234	297
141	8	7805	8938	emb|Z49988|SPMM	Streptococcus pneumoniae mmsA gene	99	338	1134
141	9	8936	10972	emb|Z49988|SPMM	Streptococcus pneumoniae mmsA gene	99	2037	2037
141	10	11472	12467	emb|Z49988|SPMM	Streptococcus pneumoniae mmsA gene	100	76	996
142	2	257	814	gb|M80215|	Streptococcus pneumoniae uvs402 protein gene, complete cds	98	174	558
142	3	787	957	gb|M80215|	Streptococcus pneumoniae uvs402 protein gene, complete cds	100	142	171
142	4	980	3022	gb|M80215|	Streptococcus pneumoniae uvs402 protein gene, complete cds	95	1997	2043

TABLE 1

S. pneumoniae - Coding regions containing known sequences

<table>
<tr><th>Contig ID</th><th>ORF ID</th><th>Start (nt)</th><th>Stop (nt)</th><th>match acession</th><th>match gene name</th><th>percent ident</th><th>HSP nt length</th><th>ORF nt length</th></tr>
<tr><td>142</td><td>5</td><td>3020</td><td>3595</td><td>gb|M80215|</td><td>Streptococcus pneumoniae uvs402 protein gene, complete cds</td><td>100</td><td>153</td><td>576</td></tr>
<tr><td>145</td><td>1</td><td>1</td><td>219</td><td>emb|Z35135|SPAL</td><td>S.pneumoniae aliA gene for amiA-like gene A</td><td>97</td><td>185</td><td>219</td></tr>
<tr><td>145</td><td>2</td><td>171</td><td>1994</td><td>gb|L20556|</td><td>Streptococcus pneumoniae plpA gene, partial cds</td><td>99</td><td>1811</td><td>1824</td></tr>
<tr><td>145</td><td>3</td><td>2287</td><td>7599</td><td>emb|Z47210|SPDE</td><td>S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs</td><td>99</td><td>1052</td><td>5313</td></tr>
<tr><td>145</td><td>4</td><td>9934</td><td>7766</td><td>gb|M90527|</td><td>Streptococcus pneumoniae penicillin-binding protein (ponA) gene, complete cds</td><td>99</td><td>2169</td><td>2169</td></tr>
<tr><td>145</td><td>5</td><td>10488</td><td>9922</td><td>gb|M90527|</td><td>Streptococcus pneumoniae penicillin-binding protein (ponA) gene, complete cds</td><td>99</td><td>512</td><td>567</td></tr>
<tr><td>146</td><td>1</td><td>159</td><td>4</td><td>emb|Z82002|SPZ8</td><td>S.pneumoniae pcpB and pcpC genes</td><td>98</td><td>156</td><td>156</td></tr>
<tr><td>146</td><td>2</td><td>344</td><td>90</td><td>emb|Z82002|SPZ8</td><td>S.pneumoniae pcpB and pcpC genes</td><td>98</td><td>255</td><td>255</td></tr>
<tr><td>146</td><td>16</td><td>11795</td><td>10794</td><td>emb|Z82002|SPZ8</td><td>S.pneumoniae pcpB and pcpC genes</td><td>85</td><td>276</td><td>1002</td></tr>
<tr><td>147</td><td>11</td><td>10678</td><td>10202</td><td>emb|Z21702|SPUN</td><td>S.pneumoniae ung gene and mutX genes encoding uracil-DNA glycosylase and 8-oxodGTP nucleoside triphosphatase</td><td>98</td><td>477</td><td>477</td></tr>
<tr><td>147</td><td>12</td><td>11338</td><td>10676</td><td>emb|Z21702|SPUN</td><td>S.pneumoniae ung gene and mutX genes encoding uracil-DNA glycosylase and 8-oxodGTP nucleoside triphosphatase</td><td>99</td><td>663</td><td>663</td></tr>
<tr><td>148</td><td>12</td><td>9009</td><td>8815</td><td>gb|U41735|</td><td>Streptococcus pneumoniae peptide methionine sulfoxide reductase (msrA) and homoserine kinase homolog (thrB) genes, complete cds</td><td>90</td><td>180</td><td>195</td></tr>
<tr><td>156</td><td>4</td><td>1154</td><td>1402</td><td>emb|X63602|SPBO</td><td>S.pneumoniae mmsA-Box</td><td>94</td><td>185</td><td>249</td></tr>
<tr><td>159</td><td>13</td><td>9048</td><td>8521</td><td>gb|M36180|</td><td>Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds</td><td>98</td><td>526</td><td>528</td></tr>
<tr><td>160</td><td>1</td><td>1</td><td>147</td><td>emb|Z26851|SPAT</td><td>S.pneumoniae (R6) genes for ATPase a subunit, ATPase b subunit and ATPase c subunit</td><td>100</td><td>142</td><td>147</td></tr>
<tr><td>160</td><td>2</td><td>179</td><td>898</td><td>emb|Z26851|SPAT</td><td>S.pneumoniae (R6) genes for ATPase a subunit, ATPase b subunit and ATPase c subunit</td><td>99</td><td>720</td><td>720</td></tr>
<tr><td>160</td><td>3</td><td>906</td><td>1406</td><td>emb|Z26850|SPAT</td><td>S.pneumoniae (M222) genes for ATPase a subunit, ATPase b subunit and ATPase c subunit</td><td>95</td><td>501</td><td>501</td></tr>
<tr><td>160</td><td>4</td><td>1373</td><td>1942</td><td>emb|Z26850|SPAT</td><td>S.pneumoniae (M222) genes for ATPase a subunit, ATPase b subunit and ATPase c subunit</td><td>87</td><td>306</td><td>570</td></tr>
<tr><td>161</td><td>1</td><td>1</td><td>984</td><td>emb|X77249|SPR6</td><td>S.pneumoniae (R6) ciaR/ciaH genes</td><td>99</td><td>984</td><td>984</td></tr>
<tr><td>161</td><td>7</td><td>6910</td><td>7497</td><td>emb|X83917|SPGY</td><td>S.pneumoniae orf1gyrB and gyrB gene encoding DNA gyrase B subunit</td><td>99</td><td>437</td><td>588</td></tr>
<tr><td>161</td><td>8</td><td>7443</td><td>9386</td><td>emb|X83917|SPGY</td><td>S.pneumoniae orf1gyrB and gyrB gene encoding DNA gyrase B subunit</td><td>98</td><td>1912</td><td>1944</td></tr>
<tr><td>163</td><td>1</td><td>2</td><td>2155</td><td>gb|L20559|</td><td>Streptococcus pneumoniae Exp5 gene, partial cds</td><td>98</td><td>327</td><td>2154</td></tr>
</table>

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
165	1	32	1618	gb|J01796|	S.pneumoniae malX and malM genes encoding membrane protein and amylomaltase, complete cds, and malP gene encoding phosphorylase	99	1587	1587
165	2	1608	3902	gb|J01796|	S.pneumoniae malX and malM genes encoding membrane protein and amylomaltase, complete cds, and malP gene encoding phosphorylase	100	280	2295
166	1	378	4	emb|Y11463|SPDN	Streptococcus pneumoniae dnaG, rpoD, cpoA genes and ORF3 and ORF5	100	375	375
166	2	1507	320	emb|Y11463|SPDN	Streptococcus pneumoniae dnaG, rpoD, cpoA genes and ORF3 and ORF5	99	1188	1188
166	3	3240	1432	emb|Y11463|SPDN	Streptococcus pneumoniae dnaG, rpoD, cpoA genes and ORF3 and ORF5	99	563	1809
167	1	1077	328	emb|Z71552|SPAD	Streptococcus pneumoniae adcCBA operon	94	155	750
167	2	1844	999	emb|Z71552|SPAD	Streptococcus pneumoniae adcCBA operon	98	405	846
167	3	2714	1842	emb|Z71552|SPAD	Streptococcus pneumoniae adcCBA operon	97	604	873
167	4	3399	2641	emb|Z71552|SPAD	Streptococcus pneumoniae adcCBA operon	99	703	759
168	1	1	2259	gb|L20558|	Streptococcus pneumoniae Exp4 gene, partial cds	99	282	2259
170	10	7338	7685	emb|Z77726|SPIS	S.pneumoniae DNA for insertion sequence IS1318 (1372 bp)	95	315	348
172	6	2462	4981	gb|U47625|	Streptococcus pneumoniae formate acetyltransferase (exp72) gene, partial cds	97	365	2520
175	1	373	20	gb|M36180|	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	89	353	354
175	4	1843	3621	emb|Z47210|SPDE	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs	95	89	1779
176	5	3984	2980	emb|Z67739|SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	100	573	1005
178	1	3	425	emb|Z67739|SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	95	423	423
179	1	426	70	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	99	338	357
180	3	3084	1855	emb|X95718|SPGY	S.pneumoniae gyrA gene	99	381	1230
186	1	714	4	emb|Z79691|SOOR	S.pneumoniae yorf[A,B,C,D,E], ftsL, pbpX and regR genes	98	59	711
186	2	2254	608	emb|Z79691|SOOR	S.pneumoniae yorf[A,B,C,D,E], ftsL, pbpX and regR genes	98	315	1647
186	3	707	880	emb|Z79691|SOOR	S.pneumoniae yorf[A,B,C,D,E], ftsL, pbpX and regR genes	98	174	174
189	1	2	259	gb|U72720|	Streptococcus pneumoniae heat shock protein 70 (dnaK) gene, complete cds and DnaJ (dnaJ) gene, partial cds	99	258	258
189	2	600	385	gb|U72720|	Streptococcus pneumoniae heat shock protein 70 (dnaK) gene, complete cds and DnaJ (dnaJ) gene, partial cds	98	204	216

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
189	3	1018	851	gb|U72720|	Streptococcus pneumoniae heat shock protein 70 (dnaK) gene, complete cds and DnaJ (dnaJ) gene, partial cds	99	168	168
189	4	1012	2154	gb|U72720|	Streptococcus pneumoniae heat shock protein 70 (dnaK) gene, complete cds and DnaJ (dnaJ) gene, partial cds	99	1062	1143
191	9	7829	7524	emb|X63602|SPBO	S.pneumoniae mmsA-Box	95	234	306
194	1	1	729	gb|M36180|	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	91	728	729
199	2	1117	881	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	96	211	237
199	4	1499	1762	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	89	248	264
199	5	1781	2284	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	98	504	504
203	1	1977	337	gb|L20563|	Streptococcus pneumoniae Exp9 gene, partial cds	99	342	1641
204	1	1145	3	gb|L36131|	Streptococcus pneumoniae exp10 gene, complete cds, recA gene, 5′ end	99	1143	1143
208	1	59	2296	gb|U89711|	Streptococcus pneumoniae pneumococcal surface protein A PspA (pspA) gene, complete cds	90	471	2238
213	3	2455	2123	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	96	332	333
216	1	368	12	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	99	338	357
216	3	2650	2327	gb|M28678|	S.pneumoniae promoter sequence DNA	98	86	324
222	1	417	4	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	94	414	414
227	3	5266	4238	emb|AJ000336|SP	Streptococcus pneumoniae ldh gene	99	1029	1029
239	1	1	804	gb|M31296|	S.pneumoniae recP gene, complete cds	95	484	804
247	3	1625	1807	gb|M36180|	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	94	178	183
249	3	921	1364	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	94	443	444
253	1	362	3	gb|M36180|	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	99	360	360
253	5	1238	2050	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	95	420	813

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
253	6	2069	2572	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	97	504	504
255	1	3	800	emb|Z82002|SPZ8	S.pneumoniae pcpB and pcpC genes	97	531	798
255	2	798	1841	emb|Z82002|SPZ8	S.pneumoniae pcpB and pcpC genes	97	672	1044
255	3	2493	1969	emb|Z67739|SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	92	435	525
257	2	985	770	emb|X17337|SPAM	Streptococcus pneumoniae ami locus conferring aminopterin resistance	96	117	216
257	3	1245	907	gb|M36180|	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	97	339	339
267	2	495	1208	gb|U16156|	Streptococcus pneumoniae dihydropteroate synthase (sulA), dihydrofolate synthetase (sulB), guanosine triphosphate cyclohydrolase (sulC), aldolase-pyrophosphokinase (sulD) genes, complete cds	95	84	714
267	3	1291	2277	gb|U16156|	Streptococcus pneumoniae dihydropteroate synthase (sulA), dihydrofolate synthetase (sulB), guanosine triphosphate cyclohydrolase (sulC), aldolase-pyrophosphokinase (sulD) genes, complete cds	97	755	987
267	4	2261	3601	gb|U16156|	Streptococcus pneumoniae dihydropteroate synthase (sulA), dihydrofolate synthetase (sulB), guanosine triphosphate cyclohydrolase (sulC), aldolase-pyrophosphokinase (sulD) genes, complete cds	98	1341	1341
267	5	3561	4136	gb|U16156|	Streptococcus pneumoniae dihydropteroate synthase (sulA), dihydrofolate synthetase (sulB), guanosine triphosphate cyclohydrolase (sulC), aldolase-pyrophosphokinase (sulD) genes, complete cds	99	576	576
267	6	4164	4949	gb|U16156|	Streptococcus pneumoniae dihydropteroate synthase (sulA), dihydrofolate synthetase (sulB), guanosine triphosphate cyclohydrolase (sulC), aldolase-pyrophosphokinase (sulD) genes, complete cds	99	748	786
267	7	5544	5140	gb|U16156|	Streptococcus pneumoniae dihydropteroate synthase (sulA), dihydrofolate synthetase (sulB), guanosine triphosphate cyclohydrolase (sulC), aldolase-pyrophosphokinase (sulD) genes, complete cds	100	186	405
268	4	1793	1990	emb|X63602|SPBO	S.pneumoniae mmsA-Box	89	194	198
271	1	562	104	gb|M29686|	S.pneumoniae mismatch repair (hexB) gene, complete cds	93	160	459
291	1	75	524	gb|U04047|	Streptococcus pneumoniae SSZ dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	96	450	450
291	2	1001	525	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	87	205	477
291	3	807	559	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	90	170	249
291	4	1374	1099	gb|M36180|	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	85	264	276

TABLE 1 S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
293	1	3	1673	emb|Z67740|SPGY	S.pneumoniae gyrB gene and unknown orf	98	553	1671
296	1	1434	151	emb|Z47210|SPDE	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs	99	430	1284
317	1	157	510	emb|Z67739|SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	89	353	354
325	2	1237	485	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	91	299	753
326	1	1	462	emb|Z82001|SPZ8	S.pneumoniae pcpA gene and open reading frames	100	233	462
327	1	603	64	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	94	89	540
334	1	153	545	gb|U41735|	Streptococcus pneumoniae peptide methionine sulfoxide reductase (msrA) and homoserine kinase homolog (thrB) genes, complete cds	87	91	393
336	1	308	93	emb|Z26850|SPAT	S.pneumoniae (M222) genes for ATPase a subunit, ATPase b subunit and ATPase c subunit	97	102	216
360	1	1	519	emb|Z67739|SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	95	435	519
360	4	1598	1960	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	94	353	363
362	1	673	2	emb|Z83335|SPZ8	S.pneumoniae dexB, cap1[A,B,C,D,E,F,G,H,I,J,K] genes, dTDP-rhamnose biosynthesis genes and aliA gene	95	63	672
362	2	1168	728	gb|U04047|	Streptococcus pneumoniae SSZ dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	96	441	441
384	1	347	111	emb|X85787|SPCP	S.pneumoniae dexB, cps14A, cps14B, cps14C, cps14D, cps14E, cps14F, cps14G, cps14H, cps14I, cps14J, cps14K, cps14L, tasA genes	94	54	237

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
228	2	1760	1942	pir|F60663|F606	translation elongation factor Tu - Streptococcus oralis	100	100	183
319	1	2	205	gi|984927	neomycin phosphotransferase [Cloning vector pBSL99]	100	100	204
260	1	2	1138	pir|F60663|F606	translation elongation factor Tu - Streptococcus oralis	99	98	1137
25	2	486	1394	gi|1574495	hypothetical [Haemophilus influenzae]	98	96	909
94	2	685	1002	gi|310627	phosphoenolpyruvate:sugar phosphotransferase system HPr [Streptococcus mutans]	98	93	318
312	1	190	2	gi|347999	ATP-dependent protease proteolytic subunit [Streptococcus salivarius]	98	95	189
329	1	1	807	gi|924848	inosine monophosphate dehydrogenase [Streptococcus pyogenes]	98	94	807
336	2	290	589	gi|987050	lacZ gene product [unidentified cloning vector]	98	98	300
181	9	5948	7366	gi|153755	phospho-beta-D-galactosidase (EC 3.2.1.85) [Lactococcus lactis cremoris]	97	94	1419
312	2	1044	361	gi|347998	uracil phosphoribosyltransferase [Streptococcus salivarius]	97	88	684
32	8	6575	7486	sp|P37214|ERA_S	GTP-BINDING PROTEIN ERA HOMOLOG.	96	91	912
94	3	951	2741	gi|153615	phosphoenolpyruvate:sugar phosphotransferase system enzyme I [Streptococcus salivarius]	96	92	1791
127	1	1	168	gi|581299	initiation factor IF-1 [Lactococcus lactis]	96	89	168
128	14	10438	11154	gi|1276873	DeoD [Streptococcus thermophilus]	96	93	717
181	4	1362	1598	gi|46606	lacD polypeptide (AA 1-326) [Staphylococcus aureus]	96	80	237
218	1	1	834	gi|1743856	intrageneric coaggregation-relevant adhesin [Streptococcus gordonii]	96	93	834
319	2	115	441	gi|208225	heat-shock protein 82/neomcyn phosphotransferase fusion protein (hsp82-neo) [unidentified cloning vector]	96	96	327
54	12	8622	10967	gnl|PID|d100972	Pyruvate formate-lyase [Streptococcus mutans]	95	89	2346
181	2	606	1289	gi|149396	lacD [Lactococcus lactis]	95	89	684
46	3	3410	3045	gi|1850606	YlxM [Streptococcus mutans]	94	86	366
89	10	7972	7337	gi|703442	thymidine kinase [Streptococcus gordonii]	94	86	636
148	9	6431	7354	gi|995767	UDP-glucose pyrophosphorylase [Streptococcus pyogenes]	94	85	924
160	7	4430	5848	gi|153573	H+ ATPase [Enterococcus faecalis]	94	87	1419
2	3	4598	3513	gi|153763	plasmin receptor [Streptococcus pyogenes]	93	86	1086
12	8	7877	6204	gi|1103865	formyl-tetrahydrofolate synthetase [Streptococcus mutans]	93	84	1674

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

<table>
<tr><th>Contig ID</th><th>ORF ID</th><th>Start (nt)</th><th>Stop (nt)</th><th>match acession</th><th>match gene name</th><th>% sim</th><th>% ident</th><th>length (nt)</th></tr>
<tr><td>65</td><td>11</td><td>4734</td><td>5120</td><td>gi|40150</td><td>L14 protein (AA 1-122) [Bacillus subtilis]</td><td>93</td><td>87</td><td>387</td></tr>
<tr><td>68</td><td>1</td><td>53</td><td>1297</td><td>gi|47341</td><td>antitumor protein [Streptococcus pyogenes]</td><td>93</td><td>87</td><td>1245</td></tr>
<tr><td>80</td><td>1</td><td>3</td><td>299</td><td>gnl|PID|d101166</td><td>ribosomal protein S7 [Bacillus subtilis]</td><td>93</td><td>84</td><td>297</td></tr>
<tr><td>127</td><td>3</td><td>695</td><td>1093</td><td>gi|142462</td><td>ribosomal protein S11 [Bacillus subtilis]</td><td>93</td><td>86</td><td>399</td></tr>
<tr><td>160</td><td>5</td><td>1924</td><td>3462</td><td>gi|1773264</td><td>ATPase, alpha subunit [Streptococcus mutans]</td><td>93</td><td>85</td><td>1539</td></tr>
<tr><td>211</td><td>5</td><td>3757</td><td>3047</td><td>gi|535273</td><td>aminopeptidase C [Streptococcus thermophilus]</td><td>93</td><td>82</td><td>711</td></tr>
<tr><td>262</td><td>1</td><td>16</td><td>564</td><td>gi|149394</td><td>lacB [Lactococcus lactis]</td><td>93</td><td>90</td><td>549</td></tr>
<tr><td>366</td><td>1</td><td>197</td><td>3</td><td>gi|295259</td><td>tryptophan synthase beta subunit [Synechocystis sp.]</td><td>93</td><td>91</td><td>195</td></tr>
<tr><td>25</td><td>3</td><td>1392</td><td>1976</td><td>gi|1574496</td><td>hypothetical [Haemophilus influenzae]</td><td>92</td><td>80</td><td>585</td></tr>
<tr><td>36</td><td>21</td><td>20781</td><td>19927</td><td>gi|310632</td><td>hydrophobic membrane protein [Streptococcus gordonii]</td><td>92</td><td>86</td><td>855</td></tr>
<tr><td>181</td><td>3</td><td>1265</td><td>1534</td><td>gi|149396</td><td>lacD [Lactococcus lactis]</td><td>92</td><td>83</td><td>270</td></tr>
<tr><td>181</td><td>7</td><td>3662</td><td>4060</td><td>gi|149410</td><td>enzyme III [Lactococcus lactis]</td><td>92</td><td>83</td><td>399</td></tr>
<tr><td>32</td><td>4</td><td>5631</td><td>3937</td><td>gnl|PID|e294090</td><td>fibronectin-binding protein-like protein A [Streptococcus gordonii]</td><td>91</td><td>85</td><td>1695</td></tr>
<tr><td>46</td><td>2</td><td>3054</td><td>1462</td><td>gi|1850607</td><td>signal recognition particle Ffh [Streptococcus mutans]</td><td>91</td><td>84</td><td>1593</td></tr>
<tr><td>65</td><td>10</td><td>4442</td><td>4726</td><td>pir|S17865|S178</td><td>ribosomal protein S17 - Bacillus stearothermophilus</td><td>91</td><td>80</td><td>285</td></tr>
<tr><td>77</td><td>2</td><td>260</td><td>1900</td><td>gi|287871</td><td>groEL gene product [Lactococcus lactis]</td><td>91</td><td>82</td><td>1641</td></tr>
<tr><td>84</td><td>1</td><td>2</td><td>2056</td><td>gi|871784</td><td>Clp-like ATP-dependent protease binding subunit [Bos taurus]</td><td>91</td><td>79</td><td>2055</td></tr>
<tr><td>99</td><td>8</td><td>10750</td><td>9272</td><td>gi|153740</td><td>sucrose phosphorylase [Streptococcus mutans]</td><td>91</td><td>84</td><td>1479</td></tr>
<tr><td>99</td><td>9</td><td>11947</td><td>11072</td><td>gi|153739</td><td>membrane protein [Streptococcus mutans]</td><td>91</td><td>78</td><td>876</td></tr>
<tr><td>127</td><td>5</td><td>2065</td><td>2469</td><td>pir|S07223|R5BS</td><td>ribosomal protein L17 - Bacillus stearothermophilus</td><td>91</td><td>78</td><td>405</td></tr>
<tr><td>132</td><td>6</td><td>9539</td><td>9390</td><td>gi|143065</td><td>hubst [Bacillus stearothermophilus]</td><td>91</td><td>89</td><td>150</td></tr>
<tr><td>137</td><td>8</td><td>4765</td><td>6153</td><td>gnl|PID|d100347</td><td>Na+ -ATPase beta subunit [Enterococcus hirae]</td><td>91</td><td>79</td><td>1389</td></tr>
<tr><td>151</td><td>7</td><td>11119</td><td>9734</td><td>gi|1815634</td><td>glutamine synthetase type 1 [Streptococcus agalactiae]</td><td>91</td><td>82</td><td>1386</td></tr>
<tr><td>201</td><td>2</td><td>1798</td><td>278</td><td>gi|2208998</td><td>dextran glucosidase DexS [Streptococcus suis]</td><td>91</td><td>79</td><td>1521</td></tr>
<tr><td>222</td><td>2</td><td>673</td><td>1839</td><td>gi|153741</td><td>ATP-binding protein [Streptococcus mutans]</td><td>91</td><td>85</td><td>1167</td></tr>
<tr><td>293</td><td>5</td><td>4113</td><td>4400</td><td>gi|1196921</td><td>unknown protein [Insertion sequence IS861]</td><td>91</td><td>71</td><td>288</td></tr>
<tr><td>32</td><td>7</td><td>6166</td><td>6570</td><td>pir|A36933|A369</td><td>diacylglycerol kinase homolog - Streptococcus mutans</td><td>90</td><td>77</td><td>405</td></tr>
</table>

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
33	2	841	527	gi|1196921	unknown protein [Insertion sequence IS861]	90	70	315
48	27	20908	19757	gnl|PID|e274705	lactate oxidase [Streptococcus iniae]	90	80	1152
55	21	19777	18515	gnl|PID|e221213	ClpX protein [Bacillus subtilis]	90	75	1263
56	2	717	977	gi|1710133	flagellar filament cap [Borrelia burgdorferi]	90	50	261
65	1	1	606	gi|1165303	L3 [Bacillus subtilis]	90	75	606
114	1	2	988	gi|153562	aspartate beta-semialdehyde dehydrogenase (EC 1.2.1.11) [Streptococcus mutans]	90	80	987
120	1	1345	827	gi|407880	ORF1 [Streptococcus equisimilis]	90	75	519
159	12	7690	8298	gi|143012	GMP synthetase [Bacillus subtilis]	90	84	609
166	4	4076	3282	gi|1661179	high affinity branched chain amino acid transport protein [Streptococcus mutans]	90	78	795
183	1	28	1395	gi|308858	ATP:pyruvate 2-O-phosphotransferase [Lactococcus lactis]	90	76	1368
191	3	2891	1662	gi|149521	tryptophan synthase beta subunit [Lactococcus lactis]	90	78	1230
198	2	1551	436	gi|2323342	(AF014460) CcpA [Streptococcus mutans]	90	76	1116
305	1	37	783	gi|1573551	asparagine synthetase A (asnA) [Haemophilus influenzae]	90	80	747
8	3	2285	3343	gi|149434	putative [Lactococcus lactis]	89	78	1059
46	8	7577	7362	pir|A45434|A454	ribosomal protein L19 - Bacillus stearothermophilus	89	76	216
49	9	8363	10342	gi|153792	recP peptide [Streptococcus pneumoniae]	89	83	1980
51	14	18410	19447	gi|308857	ATP:D-fructose 6-phosphate 1-phosphotransferase [Lactococcus lactis]	89	81	1038
57	11	9686	10669	gnl|PID|d100932	H2O-forming NADH Oxidase [Streptococcus mutans]	89	77	984
65	5	2418	2786	gi|1165307	S19 [Bacillus subtilis]	89	81	369
65	8	3806	4225	sp|P14577|RL16_	50S RIBOSOMAL PROTEIN L16.	89	82	420
65	18	8219	8719	gi|143417	ribosomal protein S5 [Bacillus stearothermophilus]	89	76	501
73	9	6337	5315	gi|532204	prs [Listeria monocytogenes]	89	70	1023
76	3	3360	1465	gnl|PID|e200671	lepA gene product [Bacillus subtilis]	89	76	1896
99	10	12818	11919	gi|153738	membrane protein [Streptococcus mutans]	89	73	900
120	2	3552	1300	gi|407881	stringent response-like protein [Streptococcus equisimilis]	89	79	2253
122	5	4512	2791	gnl|PID|e280490	unknown [Streptococcus pneumoniae]	89	81	1722

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
176	1	669	4	gi|47394	5-oxoprolyl-peptidase [Streptococcus pyogenes]	89	78	666
177	6	3050	3934	gi|912423	putative [Lactococcus lactis]	89	71	885
181	8	4033	5751	gi|149411	enzyme III [Lactococcus lactis]	89	80	1719
211	4	3149	2793	gi|535273	aminopeptidase C [Streptococcus thermophilus]	89	83	357
361	1	431	838	gi|1196922	unknown protein [Insertion sequence IS861]	89	70	408
34	17	11839	10535	sp|P30053|SYH_S	HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE--TRNA LIGASE) (HISRS).	88	78	1305
38	3	1646	2623	gi|2058544	putative ABC transporter subunit ComYA [Streptococcus gordonii]	88	78	978
54	1	3	227	gnl|PID|d101320	YqgU [Bacillus subtilis]	88	66	225
57	2	611	1468	gnl|PID|e134943	putative reductase 1 [Saccharomyces cerevisiae]	88	75	858
65	13	5497	6069	pir|A29102|R5BS	ribosomal protein L5 - Bacillus stearothermophilus	88	75	573
65	20	9030	9500	gi|2078381	ribosomal protein L15 [Staphylococcus aureus]	88	83	471
78	3	3636	1108	gnl|PID|d100781	lysyl-aminopeptidase [Lactococcus lactis]	88	80	2529
106	12	12965	12054	gi|2407215	(AF017421) putative heat shock protein HtpX [Streptococcus gordonii]	88	72	912
107	2	219	962	gnl|PID|e339862	putative acylneuraminate lyase [Clostridium tertium]	88	75	744
111	8	14073	10420	gi|402363	RNA polymerase beta-subunit [Bacillus subtilis]	88	74	3654
126	9	13096	12062	gnl|PID|e311468	unknown [Bacillus subtilis]	88	74	1035
140	17	19143	18874	gi|1573659	H. influenzae predicted coding region HI0659 [Haemophilus influenzae]	88	61	270
144	1	394	555	gnl|PID|e274705	lactate oxidase [Streptococcus iniae]	88	75	162
148	4	2723	3493	gi|1591672	phosphate transport system ATP-binding protein [Methanococcus jannaschii]	88	68	771
160	8	5853	6278	gi|1773267	ATPase, epsilon subunit [Streptococcus mutans]	88	65	426
177	4	1770	2885	gi|149426	putative [Lactococcus lactis]	88	72	1116
211	6	4140	3613	gi|535273	aminopeptidase C [Streptococcus thermophilus]	88	74	528
231	4	580	957	gi|40186	homologous to E.coli ribosomal protein L27 [Bacillus subtilis]	88	78	378
260	5	2387	2998	gi|1196922	unknown protein [Insertion sequence IS861]	88	69	612
291	6	2017	3375	gnl|PID|d100571	adenylosuccinate synthetase [Bacillus subtilis]	88	75	1359
319	4	658	317	gi|603578	serine/threonine kinase [Phytophthora capsici]	88	88	342
40	5	4353	4514	gi|153672	lactose repressor [Streptococcus mutans]	87	56	162

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
49	10	10660	10929	gi|1196921	unknown protein [Insertion sequence IS861]	87	72	270
65	7	3140	3808	gi|1165309	S3 [Bacillus subtilis]	87	73	669
65	15	6623	7039	gi|1044978	ribosomal protein S8 [Bacillus subtilis]	87	73	417
75	8	5411	6625	gi|1877422	galactokinase [Streptococcus mutans]	87	78	1215
80	2	703	2805	gnl|PID|d101166	elongation factor G [Bacillus subtilis]	87	76	2103
82	1	541	248	gi|1196921	unknown protein [Insertion sequence IS861]	87	69	294
140	23	25033	23897	gnl|PID|e254999	phenylalany-tRNA synthetase beta subunit [Bacillus subtilis]	87	74	1137
214	14	10441	8516	gi|2281305	glucose inhibited division protein homolog GidA [Lactococcus lactis cremoris]	87	75	1926
220	2	2742	874	gnl|PID|e324358	product highly similar to elongation factor EF-G [Bacillus subtilis]	87	73	1869
260	4	2096	2389	gi|1196921	unknown protein [Insertion sequence IS861]	87	72	294
323	1	27	650	gi|897795	30S ribosomal protein [Pediococcus acidilactici]	87	73	624
357	1	154	570	gi|1044978	ribosomal protein S8 [Bacillus subtilis]	87	73	417
49	11	10927	11445	gi|1196922	unknown protein [Insertion sequence IS861]	86	63	519
59	12	7461	9224	gi|951051	relaxase [Streptococcus pneumoniae]	86	68	1764
65	4	1553	2401	pir|A02759|R5BS	ribosomal protein L2 - Bacillus stearothermophilus	86	77	849
65	23	10957	11610	gi|44074	adenylate kinase [Lactococcus lactis]	86	76	654
82	4	4374	4856	gi|153745	mannitol-specific enzyme III [Streptococcus mutans]	86	72	483
102	4	4270	4986	gnl|PID|e264705	OMP decarboxylase [Lactococcus lactis]	86	76	717
106	6	7824	6880	gnl|PID|e137598	aspartate transcarbamylase [Lactobacillus leichmannii]	86	68	945
107	1	1	273	gnl|PID|e339862	putative acylneuraminate lyase [Clostridium tertium]	86	71	273
111	7	10432	6710	gnl|PID|e228283	DNA-dependent RNA polymerase [Streptococcus pyogenes]	86	80	3723
131	9	5704	4892	gi|1661193	polipoprotein diacylglycerol transferase [Streptococcus mutans]	86	71	813
134	7	6430	7980	gi|2388637	glycerol kinase [Enterococcus faecalis]	86	73	1551
146	11	7473	6583	gi|1591731	melvalonate kinase [Methanococcus jannaschii]	86	72	891
153	2	595	2010	gi|2160707	dipeptidase [Lactococcus lactis]	86	78	1416
154	1	2	1435	gi|1857246	6-phosphogluconate dehydrogenase [Lactococcus lactis]	86	74	1434

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
161	5	5025	6284	gi|47529	Unknown [Streptococcus salivarius]	86	66	1260
184	1	2	1483	gi|642667	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase [Streptococcus mutans]	86	73	1482
210	8	3659	6571	gi|153661	translational initiation factor IF2 [Enterococcus faecium]	86	76	2913
250	1	2	187	gi|1573551	asparagine synthetase A (asnA) [Haemophilus influenzae]	86	68	186
36	4	2644	3909	gi|2149909	cell division protein [Enterococcus faecalis]	85	73	1266
38	4	2475	3587	gi|2058545	putative ABC transporter subunit ComYB [Streptococcus gordonii]	85	72	1113
38	5	3577	3915	gi|2058546	ComYC [Streptococcus gordonii]	85	80	339
57	5	2797	3789	gnl|PID|d101316	YqfJ [Bacillus subtilis]	85	72	993
82	5	4915	6054	gi|153746	mannitol-phosphate dehydrogenase [Streptococcus mutans]	85	68	1140
83	15	14690	15793	gi|143371	phosphoribosyl aminoimidazole synthetase (PUR-M) [Bacillus subtilis]	85	69	1104
87	2	1417	2388	gi|1184967	ScrR [Streptococcus mutans]	85	69	972
108	3	2666	3154	gi|153566	ORF (19K protein) [Enterococcus faecalis]	85	67	489
127	2	312	692	gi|1044989	ribosomal protein S13 [Bacillus subtilis]	85	72	381
128	3	1534	2409	gi|1685110	tetrahydrofolate dehydrogenase/cyclohydrolase [Streptococcus thermophilus]	85	71	876
137	7	2962	4767	gnl|PID|d100347	Na+ -ATPase alpha subunit [Enterococcus hirae]	85	74	1806
170	2	2622	709	gnl|PID|d102006	(AB001488) FUNCTION UNKNOWN, SIMILAR PRODUCT IN E.COLI, H. INFLUENZAE AND NEISSERIA MENINGITIDIS. [Bacillus subtilis]	85	70	1914
187	5	3760	4386	gi|727436	putative 20-kDa protein [Lactococcus lactis]	85	65	627
233	2	728	1873	gi|1163116	ORF-5 [Streptococcus pneumoniae]	85	67	1146
234	3	962	1255	gi|2293155	(AF008220) YtiA [Bacillus subtilis]	85	61	294
240	1	309	1931	gi|143597	CTP synthetase [Bacillus subtilis]	85	70	1623
6	1	199	1521	gi|508979	GTP-binding protein [Bacillus subtilis]	84	72	1323
10	4	4375	3443	gnl|PID|e339862	putative acylneuraminate lyase [Clostridium tertium]	84	70	933
14	1	63	2093	gi|520753	DNA topoisomerase I [Bacillus subtilis]	84	69	2031
19	4	1793	2593	gi|2352484	(AF005098) RNAseH II [Lactococcus lactis]	84	68	801
20	17	17720	19687	gnl|PID|d100584	cell division protein [Bacillus subtilis]	84	71	1968
22	28	21723	20884	gi|299163	alanine dehydrogenase [Bacillus subtilis]	84	68	840

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
30	10	7730	6792	gnl|PID|d100296	fructokinase [Streptococcus mutans]	84	75	939
33	9	5650	5300	gi|147194	phnA protein [Escherichia coli]	84	71	351
36	22	21551	20772	gi|310631	ATP binding protein [Streptococcus gordonii]	84	72	780
48	4	2837	2505	gi|882609	6-phospho-beta-glucosidase [Escherichia coli]	84	69	333
58	1	41	1516	gi|450849	amylase [Streptococcus bovis]	84	73	1476
59	10	6715	7116	gi|951053	ORF10, putative [Streptococcus pneumoniae]	84	74	402
62	1	21	644	gi|806487	ORF211; putative [Lactococcus lactis]	84	66	624
65	17	7779	8207	gi|1044980	ribosomal protein L18 [Bacillus subtilis]	84	73	429
65	21	9507	10397	gi|44073	SecY protein [Lactococcus lactis]	84	68	891
106	4	5474	2262	gnl|PID|e199387	carbamoyl-phosphate synthase [Lactobacillus plantarum]	84	73	3213
159	1	147	4	gi|806487	ORF211; putative [Lactococcus lactis]	84	63	144
163	4	4690	5910	gi|2293164	(AF008220) SAM synthase [Bacillus subtilis]	84	69	1221
192	1	46	1308	gi|495046	tripeptidase [Lactococcus lactis]	84	73	1263
348	1	671	6	gi|1787753	(AE000245) f346; 79 pct identical to 336 amino acids of ADH1_ZYMMO SW: P20368 but has 10 additional N-ter residues [Escherichia coli]	84	71	666
3	4	1572	3575	gi|143766	(thrSv) (EC 6.1.1.3) [Bacillus subtilis]	83	65	2004
9	6	3893	3417	gnl|PID|d100576	single strand DNA binding protein [Bacillus subtilis]	83	68	477
17	15	7426	8457	gi|520738	comA protein [Streptococcus pneumoniae]	83	66	1032
20	12	13860	14144	gnl|PID|d100583	unknown [Bacillus subtilis]	83	61	285
23	4	3358	2606	gi|1788294	(AE000290) o238; This 238 aa orf is 40 pct identical (5 gaps) to 231 residues of an approx. 248 aa protein YEBC_ECOLI SW: P24237 [Escherichia coli]	83	74	753
28	6	3304	3005	gi|1573659	H. influenzae predicted coding region HI0659 [Haemophilus influenzae]	83	57	300
35	7	5108	3867	gi|311707	hypothetical nucleotide binding protein [Acholeplasma laidlawii]	83	63	1242
55	19	17932	17528	gi|537085	ORF_f141 [Escherichia coli]	83	59	405
55	20	18539	17919	gi|496558	orfX [Bacillus subtilis]	83	69	621
65	6	2795	3142	gi|1165308	L22 [Bacillus subtilis]	83	64	348
68	6	6877	6683	gi|1213494	immunoglobulin A1 protease [Streptococcus pneumoniae]	83	54	195

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
87	15	15112	14771	gnl|PID|e323522	putative rpoZ protein [Bacillus subtilis]	83	54	342
96	12	8963	9631	gi|47394	5-oxoprolyl-peptidase [Streptococcus pyogenes]	83	73	669
98	1	3	263	gi|1183885	glutamine-binding subunit [Bacillus subtilis]	83	55	261
120	4	7170	5233	gi|310630	zinc metalloprotease [Streptococcus gordonii]	83	72	1938
127	7	2998	4347	gi|1500567	M. jannaschii predicted coding region MJ1665 [Methanococcus jannaschii]	83	72	1350
137	1	3	440	gi|472918	v-type Na-ATPase [Enterococcus hirae]	83	60	438
160	6	3466	4356	gi|1773265	ATPase, gamma subunit [Streptococcus mutans]	83	67	891
214	4	2278	2964	gi|663279	transposase [Streptococcus pneumoniae]	83	72	687
226	3	2367	2020	gi|142154	thioredoxin [Synechococcus PCC6301]	83	58	348
303	1	3	1049	gi|40046	phosphoglucose isomerase A (AA 1-449) [Bacillus stearothermophilus]	83	67	1047
303	2	1155	1931	gi|289282	glutamyl-tRNA synthetase [Bacillus subtilis]	83	67	777
6	17	15370	14318	gi|633147	ribose-phosphate pyrophosphokinase [Bacillus caldolyticus]	82	64	1053
7	1	299	96	gi|143648	ribosomal protein L28 [Bacillus subtilis]	82	69	204
9	3	1479	1090	gi|385178	unknown [Bacillus subtilis]	82	46	390
9	7	4213	3899	gnl|PID|d100576	ribosomal protein S6 [Bacillus subtilis]	82	60	315
12	6	4688	3942	gnl|PID|d100571	unknown [Bacillus subtilis]	82	68	747
22	17	13422	14837	gi|520754	putative [Bacillus subtilis]	82	69	1416
22	18	14897	15658	gnl|PID|d101929	uridine monophosphate kinase [Synechocystis sp.]	82	62	762
33	16	11471	10641	gnl|PID|d101190	ORF4 [Streptococcus mutans]	82	68	831
35	9	7400	6255	gi|1881543	UDP-N-acetylglucosamine-2-epimerase [Streptococcus pneumoniae]	82	68	1146
40	10	8003	7533	gi|1173519	riboflavin synthase beta subunit [Actinobacillus pleuropneumoniae]	82	68	471
48	32	23159	23437	gi|1930092	outer membrane protein [Campylobacter jejuni]	82	61	279
52	14	13833	14765	gi|142521	deoxyribodipyrimidine photolyase [Bacillus subtilis]	82	61	933
60	4	4737	1849	gnl|PID|d102221	(AB001610) uvrA [Deinococcus radiodurans]	82	66	2889
62	4	2131	1457	gi|2246749	(AF009622) thioredoxin reductase [Listeria monocytogenes]	82	63	675
71	11	16586	17518	gnl|PID|e322063	ss-1,4-galactosyltransferase [Streptococcus pneumoniae]	82	60	933
73	13	9222	7837	gnl|PID|d100586	unknown [Bacillus subtilis]	82	65	1386

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
74	1	1	3771	gnl|PID|d101199	alkaline amylopullulanase [Bacillus sp.]	82	68	3771
83	9	3696	3983	gnl|PID|e305362	unnamed protein product [Streptococcus thermophilus]	82	52	288
86	11	10776	9394	gi|683583	5-enolpyruvylshikimate-3-phosphate synthase [Lactococcus lactis]	82	67	1383
89	12	8295	9752	gi|40025	homologous to E.coli 50K [Bacillus subtilis]	82	66	1458
115	9	10347	8812	gnl|PID|d102090	(AB003927) phospho-beta-galactosidase 1 [Lactobacillus gasseri]	82	74	1536
118	1	1	1332	gnl|PID|d100579	seryl-tRNA synthetase [Bacillus subtilis]	82	71	1332
151	3	4657	6246	pir|S06097|S060	type I site-specific deoxyribonuclease (EC 3.1.21.3) CfrA chain S - Citrobacter freundii	82	66	1590
173	6	4183	3503	gi|2313836	(AE000584) conserved hypothetical protein [Helicobacter pylori]	82	68	681
177	12	5481	7442	gnl|PID|d101999	(AB001341) NcrB [Escherichia coli]	82	58	1962
193	2	178	576	pir|S08564|R3BS	ribosomal protein S9 - Bacillus stearothermophilus	82	70	399
245	2	258	845	gi|146402	EcoA type I restriction-modification enzyme S subunit [Escherichia coli]	82	68	588
9	5	3400	3146	gnl|PID|d100576	ribosomal protein S18 [Bacillus subtilis]	81	66	255
16	7	7484	8413	gi|1100074	tryptophanyl-tRNA synthetase [Clostridium longisporum]	81	70	930
20	11	10308	13820	gnl|PID|d100583	transcription-repair coupling factor [Bacillus subtilis]	81	63	3513
38	2	1232	1606	gi|2058543	putative DNA binding protein [Streptococcus gordonii]	81	63	375
45	2	3061	1751	gi|460259	enolase [Bacillus subtilis]	81	67	1311
46	1	2	1267	gi|431231	uracil permease [Bacillus caldolyticus]	81	61	1266
48	3	2453	1440	gnl|PID|d100453	Mannosephosphate Isomerase [Streptococcus mutans]	81	70	1014
54	2	1106	336	gi|154752	transport protein [Agrobacterium tumefaciens]	81	64	771
65	22	10306	10821	gi|44073	SecY protein [Lactococcus lactis]	81	66	516
89	4	3874	2603	gi|556886	serine hydroxymethyltransferase [Bacillus subtilis]	81	69	1272
99	16	19126	18929	gi|2313526	(AE000557) H. pylori predicted coding region HP0411 [Helicobacter pylori]	81	75	198
106	7	8373	7822	gnl|PID|e199384	pyrR [Lactobacillus plantarum]	81	61	552
108	6	5054	6877	gi|1469939	group B oligopeptidase PepB [Streptococcus agalactiae]	81	66	1824
113	15	15899	18283	pir|S09411|S094	spoIIIE protein - Bacillus subtilis	81	65	2385
128	5	3359	3634	gi|1685111	orf1091 [Streptococcus thermophilus]	81	69	276

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
151	1	830	3211	gi|304896	EcoE type I restriction-modification enzyme R subunit [Escherichia coli]	81	59	2382
159	11	6722	7837	gi|2239288	GMP synthetase [Bacillus subtilis]	81	69	1116
170	1	739	458	gnl|PID|d102006	(AB001488) FUNCTION UNKNOWN. [Bacillus subtilis]	81	55	282
191	2	1759	893	gi|149522	tryptophan synthase alpha subunit [Lactococcus lactis]	81	65	867
214	3	2290	1994	gi|157587	reverse transcriptase endonuclease [Drosophila virilis]	81	43	297
217	4	4415	4008	gi|466473	cellobiose phosphotransferase enzyme II' [Bacillus stearothermophilus]	81	59	408
262	2	569	868	gi|153675	tagatose 6-P kinase [Streptococcus mutans]	81	68	300
299	1	663	4	gnl|PID|e301154	StySKI methylase [Salmonella enterica]	81	60	660
366	2	376	83	gi|149521	tryptophan synthase beta subunit [Lactococcus lactis]	81	65	294
12	10	8766	9242	gi|1216490	DNA/pantothenate metabolism flavoprotein [Streptococcus mutans]	80	64	477
17	11	6050	5748	gnl|PID|e305362	unnamed protein product [Streptococcus thermophilus]	80	67	303
17	16	8455	9066	gi|703126	leucocin A translocator [Leuconostoc gelidum]	80	59	612
18	3	2440	1613	gi|1591672	phosphate transport system ATP-binding protein [Methanococcus jannaschii]	80	58	828
27	3	4248	1579	gi|452309	valyl-tRNA synthetase [Bacillus subtilis]	80	69	2670
28	7	3671	3288	gi|1573660	H. influenzae predicted coding region HI0660 [Haemophilus influenzae]	80	63	384
32	2	902	1933	gnl|PID|e264499	dihydroorotate dehydrogenase B [Lactococcus lactis]	80	66	1032
39	1	1	1266	gnl|PID|e234078	hom [Lactococcus lactis]	80	63	1266
52	5	4363	3593	gi|1183884	ATP-binding subunit [Bacillus subtilis]	80	57	771
54	5	4550	4744	gi|2198820	(AF004225) Cux/CDP(1B1); Cux/CDP homeoprotein [Mus musculus]	80	60	195
59	11	7109	7486	gi|951052	ORF9, putative [Streptococcus pneumoniae]	80	68	378
65	3	1230	1550	pir|A02815|R5BS	ribosomal protein L23 - Bacillus stearothermophilus	80	69	321
65	12	5174	5503	pir|A02819|R5BS	ribosomal protein L24 - Bacillus stearothermophilus	80	70	330
66	9	9884	10687	gi|2313836	(AE000584) conserved hypothetical protein [Helicobacter pylori]	80	66	804
82	2	648	2438	gi|622991	mannitol transport protein [Bacillus stearothermophilus]	80	65	1791
85	1	950	630	gi|528995	polyketide synthase [Bacillus subtilis]	80	46	321
89	8	6870	5779	gi|853776	peptide chain release factor 1 [Bacillus subtilis]	80	63	1092
93	12	8718	7438	gnl|PID|d101959	hypothetical protein [Synechocystis sp.]	80	60	1281

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
106	5	6854	5751	gnl|PID|e199386	glutaminase of carbamoyl-phosphate synthase [Lactobacillus plantarum]	80	65	1104
109	2	2160	1450	gi|40056	phoP gene product [Bacillus subtilis]	80	59	711
124	9	4246	3953	gnl|PID|d102254	30S ribosomal protein S16 [Bacillus subtilis]	80	65	294
128	8	5148	6428	gi|2281308	phosphopentomutase [Lactococcus lactis cremoris]	80	66	1281
137	19	12665	11376	gi|159109	NADP-dependent glutamate dehydrogenase [Giardia intestinalis]	80	68	1290
140	19	19699	19457	gi|517210	putative transposase [Streptococcus pyogenes]	80	70	243
158	2	2474	984	gi|1877423	galactose-1-P-uridyl transferase [Streptococcus mutans]	80	65	1491
171	10	7474	7728	gi|397800	cyclophilin C-associated protein [Mus musculus]	80	60	255
181	1	2	619	gi|149395	lacC [Lactococcus lactis]	80	66	618
313	1	27	539	gi|143467	ribosomal protein S4 [Bacillus subtilis]	80	70	513
329	2	1652	858	gi|533080	RecF protein [Streptococcus pyogenes]	80	63	795
371	1	2	958	gi|442360	ClpC adenosine triphosphatase [Bacillus subtilis]	80	58	957
8	7	4312	5580	gi|149435	putative [Lactococcus lactis]	79	64	1269
23	1	1175	135	gi|1542975	AbcB [Thermoanaerobacterium thermosulfurigenes]	79	61	1041
33	14	9244	8201	gnl|PID|e253891	UDP-glucose 4-epimerase [Bacillus subtilis]	79	62	1044
36	3	1242	2633	gnl|PID|e324218	ftsA [Enterococcus hirae]	79	58	1392
38	13	7155	8378	gi|405134	acetate kinase [Bacillus subtilis]	79	58	1224
55	7	9011	8229	gi|1146234	dihydrodipicolinate reductase [Bacillus subtilis]	79	56	783
65	19	8661	8915	gi|2078380	ribosomal protein L30 [Staphylococcus aureus]	79	68	255
69	4	3678	2128	gnl|PID|e311452	unknown [Bacillus subtilis]	79	64	1551
69	9	7881	7279	gi|677850	hypothetical protein [Staphylococcus aureus]	79	59	603
72	10	8491	9783	gnl|PID|d101091	hypothetical protein [Synechocystis sp.]	79	62	1293
80	3	2906	7300	gi|143342	polymerase III [Bacillus subtilis]	79	65	4395
82	14	13326	15689	gnl|PID|e255093	hypothetical protein [Bacillus subtilis]	79	65	2364
86	13	12233	11118	gi|683582	prephenate dehydrogenase [Lactococcus lactis]	79	58	1116
92	3	940	1734	gi|537286	triosephosphate isomerase [Lactococcus lactis]	79	65	795
98	6	4023	4742	gnl|PID|d100262	LivG protein [Salmonella typhimurium]	79	63	720

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
99	12	16315	14150	gi|153736	a-galactosidase [Streptococcus mutans]	79	64	2166
107	7	5684	6406	gi|460080	D-alanine:D-alanine ligase-related protein [Enterococcus faecalis]	79	58	723
113	9	6858	8303	gi|466882	pps1; B1496_C2_189 [Mycobacterium leprae]	79	64	1446
151	10	13424	12213	gi|450686	3-phosphoglycerate kinase [Thermotoga maritima]	79	60	1212
162	2	1158	3017	gi|506700	CapD [Staphylococcus aureus]	79	67	1860
177	5	2876	3052	gi|912423	putative [Lactococcus lactis]	79	61	177
177	8	4198	4563	gi|149429	putative [Lactococcus lactis]	79	61	366
187	3	2728	2907	gnl|PID|d102002	(AB001488) FUNCTION UNKNOWN. [Bacillus subtilis]	79	53	180
189	7	3589	4350	gnl|PID|e183449	putative ATP-binding protein of ABC-type [Bacillus subtilis]	79	61	762
191	5	4249	3449	gi|149519	indoleglycerol phosphate synthase [Lactococcus lactis]	79	66	801
211	3	1805	2737	gi|147404	mannose permease subunit II-M-Man [Escherichia coli]	79	57	933
212	3	3863	3621	gnl|PID|e209004	glutaredoxin-like protein [Lactococcus lactis]	79	58	243
215	1	987	715	gi|2293242	(AF008220) arginine succinate synthase [Bacillus subtilis]	79	64	273
323	2	530	781	gi|897795	30S ribosomal protein [Pediococcus acidilactici]	79	67	252
380	1	694	2	gi|1184680	polynucleotide phosphorylase [Bacillus subtilis]	79	64	693
384	2	655	239	gi|143328	phoP protein (put.); putative [Bacillus subtilis]	79	59	417
6	3	2820	4091	gi|853767	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis]	78	62	1272
8	1	50	1786	gi|149432	putative [Lactococcus lactis]	78	63	1737
9	1	351	124	gi|897793	y98 gene product [Pediococcus acidilactici]	78	59	228
15	8	7364	8314	gnl|PID|d100585	cysteine synthetase A [Bacillus subtilis]	78	63	951
20	10	9738	10310	gnl|PID|d100583	stage V sporulation [Bacillus subtilis]	78	58	573
20	16	17165	17713	gi|49105	hypoxanthine phosphoribosyltransferase [Lactococcus lactis]	78	59	549
22	22	17388	18416	gnl|PID|d101315	YqfE [Bacillus subtilis]	78	60	1029
22	27	20971	20612	gi|299163	alanine dehydrogenase [Bacillus subtilis]	78	59	360
34	8	7407	7105	gi|41015	aspartate-tRNA ligase [Escherichia coli]	78	55	303
35	8	6257	5196	gi|1657644	Cap8E [Staphylococcus aureus]	78	60	1062

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
40	11	9287	8001	gi|1173518	GTP cyclohydrase II/ 3,4-dihydroxy-2-butanone-4-phosphate synthase [Actinobacillus pleuropneumoniae]	78	58	1287
48	31	22422	23183	gi|2314330	(AE000623) glutamine ABC transporter, ATP-binding protein (glnQ) [Helicobacter pylori]	78	58	762
52	2	2101	1430	gi|1183887	integral membrane protein [Bacillus subtilis]	78	54	672
55	14	13605	12712	gnl|PID|d102026	(AB002150) YbbP [Bacillus subtilis]	78	58	894
55	17	16637	15612	gnl|PID|e313027	hypothetical protein [Bacillus subtilis]	78	51	1026
71	14	19756	19598	gi|179764	calcium channel alpha-1D subunit [Homo sapiens]	78	57	159
74	11	15031	14018	gi|1573279	Holliday junction DNA helicase (ruvB) [Haemophilus influenzae]	78	57	1014
75	9	6623	7972	gi|1877423	galactose-1-P-uridyl transferase [Streptococcus mutans]	78	62	1350
81	12	12125	13906	gi|1573607	L-fucose isomerase (fucI) [Haemophilus influenzae]	78	66	1782
82	3	2423	4417	gi|153744	ORF X; putative [Streptococcus mutans]	78	64	1995
83	18	16926	18500	gi|143373	phosphoribosyl aminoimidazole carboxy formyl formyltransferase/inosine monophosphate cyclohydrolase (PUR-H(J)) [Bacillus subtilis]	78	63	1575
83	20	20212	20775	gi|143364	phosphoribosyl aminoimidazole carboxylase I (PUR-E) [Bacillus subtilis]	78	64	564
92	2	165	878	gnl|PID|d101190	ORF2 [Streptococcus mutans]	78	62	714
98	8	5863	6909	gi|2331287	(AF013188) release factor 2 [Bacillus subtilis]	78	63	1047
113	3	1071	2741	gi|580914	dnaZX [Bacillus subtilis]	78	64	1671
127	4	1133	2071	gi|142463	RNA polymerase alpha-core-subunit [Bacillus subtilis]	78	59	939
132	1	2782	497	gi|1561763	pullulanase [Bacteroides thetaiotaomicron]	78	58	2286
135	4	2698	3537	gi|1788036	(AE000269) NH3-dependent NAD synthetase [Escherichia coli]	78	66	840
140	24	26853	25423	gi|1100077	phospho-beta-glucosidase [Clostridium longisporum]	78	64	1431
150	5	4690	4514	gi|149464	amino peptidase [Lactococcus lactis]	78	42	177
152	1	1	795	gi|639915	NADH dehydrogenase subunit [Thunbergia alata]	78	43	795
162	4	4997	4110	gnl|PID|e323528	putative YhaP protein [Bacillus subtilis]	78	64	888
181	10	8651	7947	gi|149402	lactose repressor (lacR; alt.) [Lactococcus lactis]	78	48	705
200	4	3627	4958	gnl|PID|d100172	invertase [Zymomonas mobilis]	78	61	1332
203	3	3230	3015	gi|1174237	CycK [Pseudomonas fluorescens]	78	57	216

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

<table>
<tr><th>Contig ID</th><th>ORF ID</th><th>Start (nt)</th><th>Stop (nt)</th><th>match acession</th><th>match gene name</th><th>% sim</th><th>% ident</th><th>length (nt)</th></tr>
<tr><td>210</td><td>9</td><td>6789</td><td>7172</td><td>gi|580902</td><td>ORF6 gene product [Bacillus subtilis]</td><td>78</td><td>42</td><td>384</td></tr>
<tr><td>214</td><td>6</td><td>3810</td><td>2797</td><td>gnl|PID|d102049</td><td>P. haemolytica o-sialoglycoprotein endopeptidase; P36175 (660) transmembrane [Bacillus subtilis]</td><td>78</td><td>60</td><td>1014</td></tr>
<tr><td>214</td><td>13</td><td>6322</td><td>8163</td><td>gi|1377831</td><td>unknown [Bacillus subtilis]</td><td>78</td><td>62</td><td>1842</td></tr>
<tr><td>217</td><td>1</td><td>9</td><td>2717</td><td>gi|488430</td><td>alcohol dehydrogenase 2 [Entamoeba histolytica]</td><td>78</td><td>64</td><td>2709</td></tr>
<tr><td>222</td><td>3</td><td>2316</td><td>3098</td><td>gi|1573047</td><td>spore germination and vegetative growth protein (gerC2) [Haemophilus influenzae]</td><td>78</td><td>65</td><td>783</td></tr>
<tr><td>268</td><td>1</td><td>742</td><td>8</td><td>gi|517210</td><td>putative transposase [Streptococcus pyogenes]</td><td>78</td><td>65</td><td>735</td></tr>
<tr><td>276</td><td>1</td><td>223</td><td>753</td><td>gnl|PID|d100306</td><td>ribosomal protein L1 [Bacillus subtilis]</td><td>78</td><td>65</td><td>531</td></tr>
<tr><td>312</td><td>3</td><td>1567</td><td>1079</td><td>gi|289261</td><td>comE ORF2 [Bacillus subtilis]</td><td>78</td><td>54</td><td>489</td></tr>
<tr><td>339</td><td>1</td><td>117</td><td>794</td><td>gi|1916729</td><td>CadD [Staphylococcus aureus]</td><td>78</td><td>53</td><td>678</td></tr>
<tr><td>342</td><td>2</td><td>762</td><td>265</td><td>gi|1842439</td><td>phosphatidylglycerophosphate synthase [Bacillus subtilis]</td><td>78</td><td>59</td><td>498</td></tr>
<tr><td>383</td><td>1</td><td>737</td><td>3</td><td>gi|1184680</td><td>polynucleotide phosphorylase [Bacillus subtilis]</td><td>78</td><td>64</td><td>735</td></tr>
<tr><td>7</td><td>15</td><td>11923</td><td>11018</td><td>gi|1399855</td><td>carboxyltransferase beta subunit [Synechococcus PCC7942]</td><td>77</td><td>63</td><td>906</td></tr>
<tr><td>8</td><td>2</td><td>1698</td><td>2255</td><td>gi|149433</td><td>putative [Lactococcus lactis]</td><td>77</td><td>59</td><td>558</td></tr>
<tr><td>17</td><td>14</td><td>6948</td><td>7550</td><td>gi|520738</td><td>comA protein [Streptococcus pneumoniae]</td><td>77</td><td>60</td><td>603</td></tr>
<tr><td>30</td><td>12</td><td>9761</td><td>8967</td><td>gi|1000451</td><td>TreP [Bacillus subtilis]</td><td>77</td><td>43</td><td>795</td></tr>
<tr><td>36</td><td>14</td><td>11421</td><td>12131</td><td>gi|1573766</td><td>phosphoglyceromutase (gpmA) [Haemophilus influenzae]</td><td>77</td><td>64</td><td>711</td></tr>
<tr><td>55</td><td>3</td><td>3836</td><td>4096</td><td>gi|1708640</td><td>YeaB [Bacillus subtilis]</td><td>77</td><td>55</td><td>261</td></tr>
<tr><td>61</td><td>8</td><td>8377</td><td>8054</td><td>gi|1890649</td><td>multidrug resistance protein LmrA [Lactococcus lactis]</td><td>77</td><td>51</td><td>324</td></tr>
<tr><td>65</td><td>2</td><td>607</td><td>1254</td><td>gi|40103</td><td>ribosomal protein L4 [Bacillus stearothermophilus]</td><td>77</td><td>63</td><td>648</td></tr>
<tr><td>68</td><td>8</td><td>7509</td><td>7240</td><td>gi|47551</td><td>MRP [Streptococcus suis]</td><td>77</td><td>68</td><td>270</td></tr>
<tr><td>69</td><td>1</td><td>1083</td><td>118</td><td>gnl|PID|e311493</td><td>unknown [Bacillus subtilis]</td><td>77</td><td>57</td><td>966</td></tr>
<tr><td>77</td><td>5</td><td>4583</td><td>4026</td><td>gnl|PID|e281578</td><td>hypothetical 12.2 kd protein [Bacillus subtilis]</td><td>77</td><td>60</td><td>558</td></tr>
<tr><td>83</td><td>14</td><td>13104</td><td>14552</td><td>gi|1590947</td><td>amidophosphoribosyltransferase [Methanococcus jannaschii]</td><td>77</td><td>56</td><td>1449</td></tr>
<tr><td>94</td><td>4</td><td>3006</td><td>5444</td><td>gnl|PID|e329895</td><td>(AJ000496) cyclic nucleotide-gated channel beta subunit [Rattus norvegicus]</td><td>77</td><td>66</td><td>2439</td></tr>
<tr><td>96</td><td>11</td><td>8518</td><td>8880</td><td>gi|551879</td><td>ORF 1 [Lactococcus lactis]</td><td>77</td><td>62</td><td>363</td></tr>
<tr><td>99</td><td>11</td><td>14082</td><td>12799</td><td>gi|153737</td><td>sugar-binding protein [Streptococcus mutans]</td><td>77</td><td>61</td><td>1284</td></tr>
</table>

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
106	2	361	1176	gi|148921	LicD protein [Haemophilus influenzae]	77	51	816
108	4	3152	4030	gi|1574730	tellurite resistance protein (tehB) [Haemophilus influenzae]	77	58	879
118	4	3520	3131	gi|1573900	D-alanine permease (dagA) [Haemophilus influenzae]	77	57	390
124	4	1796	1071	gi|1573162	tRNA (guanine-N1)-methyltransferase (trmD) [Haemophilus influenzae]	77	58	726
126	4	5909	4614	gnl|PID|d101163	Srb [Bacillus subtilis]	77	62	1296
128	2	630	1373	gnl|PID|d101328	YqiZ [Bacillus subtilis]	77	58	744
130	1	1	1287	gnl|PID|e325013	hypothetical protein [Bacillus subtilis]	77	61	1287
139	5	4388	3639	gi|2293302	(AF008220) YtqA [Bacillus subtilis]	77	59	750
140	11	10931	9582	gi|289284	cysteinyl-tRNA synthetase [Bacillus subtilis]	77	64	1350
140	18	19451	19263	gi|517210	putative transposase [Streptococcus pyogenes]	77	66	189
141	2	976	1683	gnl|PID|e157887	URF5 (aa 1-573) [Drosophila yakuba]	77	50	708
141	4	2735	5293	gi|556258	secA [Listeria monocytogenes]	77	59	2559
144	2	671	2173	gnl|PID|d100585	lysyl-tRNA thynthetase [Bacillus subtilis]	77	61	1503
163	5	6412	7398	gi|511015	dihydroorotate dehydrogenase A [Lactococcus lactis]	77	62	987
164	10	7841	7074	gnl|PID|d100964	homologue of iron dicitrate transport ATP-binding protein FecE of E. coli [Bacillus subtilis]	77	52	768
191	8	7257	5791	gi|149516	anthranilate synthase alpha subunit [Lactococcus lactis]	77	57	1467
198	8	5377	5177	gi|1573856	hypothetical [Haemophilus influenzae]	77	66	201
213	1	202	462	gi|1743860	Brca2 [Mus musculus]	77	50	261
250	2	231	509	gnl|PID|e334776	YlbH protein [Bacillus subtilis]	77	60	279
289	3	1737	1276	gnl|PID|d100947	Ribosomal Protein L10 [Bacillus subtilis]	77	62	462
292	2	1399	668	gi|143004	transfer RNA-Gln synthetase [Bacillus stearothermophilus]	77	58	732
7	3	2734	1166	gnl|PID|d101824	peptide-chain-release factor 3 [Synechocystis sp.]	76	53	1569
7	23	18474	18235	gi|455157	acyl carrier protein [Cryptomonas phi]	76	57	240
9	8	5706	4342	gi|1146247	asparaginyl-tRNA synthetase [Bacillus subtilis]	76	61	1365
10	5	4531	4385	gnl|PID|e314495	hypothetical protein [Clostridium perfringens]	76	53	147
18	2	1615	842	gi|1591672	phosphate transport system ATP-binding protein [Methanococcus jannaschii]	76	56	774

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
22	37	27796	28173	gnl|PID|e13389	translation initiation factor IF3 (AA 1-172) [Bacillus stearothermophilus]	76	64	378
35	6	3869	2682	gi|1773346	Cap5G [Staphylococcus aureus]	76	61	1188
48	28	21113	21787	gi|2314328	(AE000623) glutamine ABC transporter, permease protein (glnP) [Helicobacter pylori]	76	52	675
52	12	12881	13786	gi|142521	deoxyribodipyrimidine photolyase [Bacillus subtilis]	76	58	906
55	10	11521	10571	gnl|PID|e283110	femD [Staphylococcus aureus]	76	61	951
57	8	7824	6559	gi|290561	o188 [Escherichia coli]	76	47	1266
62	5	2406	2095	gnl|PID|e313024	hypothetical protein [Bacillus subtilis]	76	59	312
65	9	4223	4441	gi|40148	L29 protein (AA 1-66) [Bacillus subtilis]	76	58	219
68	2	1328	2371	gnl|PID|e284233	anabolic ornithine carbamoyltransferase [Lactobacillus plantarum]	76	61	1044
69	8	7297	6005	gnl|PID|d101420	Pyrimidine nucleoside phosphorylase [Bacillus stearothermophilus]	76	61	1293
73	12	7839	7267	gnl|PID|e243629	unknown [Mycobacterium tuberculosis]	76	53	573
74	5	8433	7039	gnl|PID|d102048	C. thermocellum beta-glucosidase; P26208 (985) [Bacillus subtilis]	76	60	1395
80	5	7643	7936	gi|2314030	(AE000599) conserved hypothetical protein [Helicobacter pylori]	76	61	294
82	15	16019	16996	gi|1573900	D-alanine permease (dagA) [Haemophilus influenzae]	76	56	978
83	19	18616	19884	gi|143374	phosphoribosyl glycinamide synthetase (PUR-D; gtg start codon) [Bacillus subtilis]	76	60	1269
86	14	13409	12231	gi|143806	AroF [Bacillus subtilis]	76	58	1179
87	1	3	1442	gi|153804	sucrose-6-phosphate hydrolase [Streptococcus mutans]	76	59	1440
87	16	15754	15110	gnl|PID|e323500	putative Gmk protein [Bacillus subtilis]	76	56	645
93	4	1769	1539	gi|1574820	1,4-alpha-glucan branching enzyme (glgB) [Haemophilus influenzae]	76	46	231
94	1	51	365	gi|144313	6.0 kd ORF [Plasmid ColE1]	76	73	315
116	2	2151	1678	gi|153841	pneumococcal surface protein A [Streptococcus pneumoniae]	76	59	474
123	6	3442	5895	gi|1314297	ClpC ATPase [Listeria monocytogenes]	76	59	2454
126	2	2156	2932	gnl|PID|d101328	YqiZ [Bacillus subtilis]	76	61	777
128	10	6973	7797	gi|944944	purine nucleoside phosphorylase [Bacillus subtilis]	76	60	825
131	11	6186	5812	gi|1674310	(AE000058) Mycoplasma pneumoniae, MG085 homolog, from M. genitalium [Mycoplasma pneumoniae]	76	47	375

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
139	4	3641	3192	gi|2293302	(AF008220) YtqA [Bacillus subtilis]	76	53	450
140	14	14872	12536	gi|1184680	polynucleotide phosphorylase [Bacillus subtilis]	76	62	2337
143	2	2583	3905	gi|143795	transfer RNA-Tyr synthetase [Bacillus subtilis]	76	61	1323
170	6	5095	6114	gnl|PID|d100959	ycgQ [Bacillus subtilis]	76	44	1020
180	2	1927	557	gi|40019	ORF 821 (aa 1-821) [Bacillus subtilis]	76	53	1371
191	7	5815	5228	gi|551880	anthranilate synthase beta subunit [Lactococcus lactis]	76	61	588
195	3	3829	2444	gi|2149905	D-glutamic acid adding enzyme [Enterococcus faecalis]	76	60	1386
200	3	1914	3629	gi|431272	lysis protein [Bacillus subtilis]	76	58	1716
201	1	431	207	gi|2208998	dextran glucosidase DexS [Streptococcus suis]	76	57	225
214	2	1283	2380	gi|663278	transposase [Streptococcus pneumoniae]	76	55	1098
225	3	2338	3411	gi|1552775	ATP-binding protein [Escherichia coli]	76	56	1074
233	1	2	724	gi|1163115	neuraminidase B [Streptococcus pneumoniae]	76	60	723
347	1	523	38	gi|537033	ORF_f356 [Escherichia coli]	76	60	486
356	2	842	165	gi|2149905	D-glutamic acid adding enzyme [Enterococcus faecalis]	76	61	678
366	3	734	348	gi|149520	phosphoribosyl anthranilate isomerase [Lactococcus lactis]	76	69	387
5	8	12599	11484	gi|1574293	fimbrial transcription regulation repressor (pilB) [Haemophilus influenzae]	75	61	1116
6	13	12553	11894	gnl|PID|d102050	ydiH [Bacillus subtilis]	75	51	660
9	10	7282	6062	gi|142538	aspartate aminotransferase [Bacillus sp.]	75	55	1221
10	12	8080	7940	gi|149493	SCRFI methylase [Lactococcus lactis]	75	56	141
18	5	4266	3301	gnl|PID|d101319	YqgH [Bacillus subtilis]	75	52	966
22	4	1838	2728	gi|1373157	orf-X; hypothetical protein; Method: conceptual translation supplied by author [Bacillus subtilis]	75	62	891
30	11	9015	7828	gi|153801	enzyme scr-II [Streptococcus mutans]	75	64	1188
31	5	2362	2030	gi|2293211	(AF008220) putative thioredoxin [Bacillus subtilis]	75	53	333
32	9	7484	8359	gnl|PID|d100560	formamidopyrimidine-DNA glycosylase [Streptococcus mutans]	75	61	876
33	4	1735	1448	gi|413976	ipa-52r gene product [Bacillus subtilis]	75	53	288
33	10	6470	5769	gi|533105	unknown [Bacillus subtilis]	75	56	702

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
33	12	6878	7183	pir|A00205|FECL	ferredoxin [4Fe-4S] - Clostridium thermaceticum	75	56	306
36	1	181	2	gi|2088739	(AF003141) strong similarity to the FABP/P2/CRBP/CRABP family of transporters [Caenorhabditis elegans]	75	43	180
38	22	14510	15379	gi|1574058	hypothetical [Haemophilus influenzae]	75	56	870
48	33	23398	24066	gi|1930092	outer membrane protein [Campylobacter jejuni]	75	56	669
51	1	2	319	gi|43985	nifS-like gene [Lactobacillus delbrueckii]	75	55	318
51	10	8318	11683	gi|537192	CG Site No. 620; alternate gene names hs, hsp, hsr, rmx apparent frameshift in GenBank Accession Number X06545 [Escherichia coli]	75	50	3366
54	18	19566	20759	gi|666069	orf2 gene product [Lactobacillus leichmannii]	75	58	1194
57	9	8448	7822	gi|290561	o188 [Escherichia coli]	75	50	627
65	14	6072	6356	gi|606241	30S ribosomal subunit protein S14 [Escherichia coli]	75	64	285
70	4	3071	2472	gi|1256617	adenine phosphoribosyltransferase [Bacillus subtilis]	75	57	600
71	24	30399	29404	gi|1574390	C4-dicarboxylate transport protein [Haemophilus influenzae]	75	57	996
73	2	910	455	gnl|PID|e249656	YneT [Bacillus subtilis]	75	57	456
79	1	1810	491	gi|1146219	28.2% of identity to the Escherichia coli GTP-binding protein Era; putative [Bacillus subtilis]	75	59	1320
82	6	6360	6536	gi|1655715	BztD [Rhodobacter capsulatus]	75	55	177
83	6	1938	2975	gnl|PID|e323529	putative PlsX protein [Bacillus subtilis]	75	56	1038
93	11	7368	5317	gi|39989	methionyl-tRNA synthetase [Bacillus stearothermophilus]	75	58	2052
93	13	9409	8699	gi|1591493	glutamine transport ATP-binding protein Q [Methanococcus jannaschii]	75	54	711
95	1	1795	47	gnl|PID|e323510	YloV protein [Bacillus subtilis]	75	57	1749
103	2	362	1186	gnl|PID|e266928	unknown [Mycobacterium tuberculosis]	75	64	825
104	1	691	915	gi|460026	repressor protein [Streptococcus pneumoniae]	75	54	225
113	5	2951	3883	gnl|PID|d101119	ABC transporter subunit [Synechocystis sp.]	75	55	933
121	1	320	1390	gi|2145131	repressor of class I heat shock gene expression HrcA [Streptococcus mutans]	75	58	1071
127	6	2614	3000	gi|1500451	M. jannaschii predicted coding region MJ1558 [Methanococcus jannaschii]	75	44	387
137	18	10082	10687	gi|393116	P-glycoprotein 5 [Entamoeba histolytica]	75	52	606
149	11	8499	9338	gnl|PID|d100582	unknown [Bacillus subtilis]	75	55	840

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
151	6	9100	7673	gi|40467	HsdS polypeptide, part of CfrA family [Citrobacter freundii]	75	57	1428
158	1	986	3	gnl|PID|e253891	UDP-glucose 4-epimerase [Bacillus subtilis]	75	63	984
172	8	5653	6774	gi|142978	glycerol dehydrogenase [Bacillus stearothermophilus]	75	56	1122
172	9	7139	9730	gnl|PID|e268456	unknown [Mycobacterium tuberculosis]	75	58	2592
173	1	261	79	gnl|PID|e236469	C10C5.6 [Caenorhabditis elegans]	75	50	183
185	3	3066	2014	gi|1574806	spermidine/putrescine transport ATP-binding protein (potA) [Haemophilus influenzae]	75	56	1053
191	6	5235	4213	gi|149518	phosphoribosyl anthranilate transferase [Lactococcus lactis]	75	61	1023
226	2	1774	1181	gi|2314588	(AE000642) conserved hypothetical protein [Helicobacter pylori]	75	65	594
231	1	1	153	gi|40173	homolog of E.coli ribosomal protein L21 [Bacillus subtilis]	75	57	153
234	1	2	418	gi|2293259	(AF008220) YtqI [Bacillus subtilis]	75	59	417
279	1	552	151	gi|1119198	unknown protein [Bacillus subtilis]	75	50	402
291	7	3558	3827	gi|40011	ORF17 (AA 1-161) [Bacillus subtilis]	75	48	270
375	2	137	628	gi|410137	ORFX13 [Bacillus subtilis]	75	58	492
6	20	16721	17560	gi|2293323	(AF008220) YtdI [Bacillus subtilis]	74	53	840
7	6	4682	6052	gi|1354211	PET112-like protein [Bacillus subtilis]	74	60	1371
18	4	3341	2427	gnl|PID|d101319	YqgI [Bacillus subtilis]	74	54	915
21	6	5885	4800	gi|1072381	glutamyl-aminopeptidase [Lactococcus lactis]	74	59	1086
24	2	739	548	gi|2314762	(AE000655) ABC transporter, permease protein (yaeE) [Helicobacter pylori]	74	46	192
25	1	2	367	gnl|PID|d100932	H2O-forming NADH Oxidase [Streptococcus mutans]	74	63	366
38	18	11432	12964	gi|537034	ORF_o488 [Escherichia coli]	74	57	1533
48	10	8924	6669	gi|1513069	P-type adenosine triphosphatase [Listeria monocytogenes]	74	53	2256
55	11	11964	11401	gnl|PID|e283110	femD [Staphylococcus aureus]	74	64	564
61	2	1782	427	gi|2293216	(AF008220) putative UDP-N-acetylmuramate-alanine ligase [Bacillus subtilis]	74	55	1356
76	10	9414	8065	gnl|PID|d101325	YqiB [Bacillus subtilis]	74	54	1350
83	2	666	926	pir|C33496|C334	hisC homolog - Bacillus subtilis	74	55	261
86	9	8985	8080	gi|683585	prephenate dehydratase [Lactococcus lactis]	74	55	906

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
102	5	5005	5652	gi|143394	OMP-PRPP transferase [Bacillus subtilis]	74	57	648
103	5	4364	3267	gnl|PID|e323524	YloN protein [Bacillus subtilis]	74	62	1098
108	7	6864	7592	gnl|PID|e257631	methyltransferase [Lactococcus lactis]	74	56	729
131	2	478	146	gnl|PID|d101320	YqgZ [Bacillus subtilis]	74	45	333
133	2	1380	919	gnl|PID|e313025	hypothetical protein [Bacillus subtilis]	74	60	462
137	9	6167	6787	gnl|PID|d100479	Na+ -ATPase subunit D [Enterococcus hirae]	74	53	621
149	4	3008	3883	gnl|PID|d100581	high level kasgamycin resistance [Bacillus subtilis]	74	55	876
157	2	243	824	gi|1573373	methylated-DNA--protein-cysteine methyltransferase (dat1) [Haemophilus influenzae]	74	48	582
164	6	3515	4249	gi|410131	ORFX7 [Bacillus subtilis]	74	48	735
167	7	5446	5201	gi|413927	ipa-3r gene product [Bacillus subtilis]	74	55	246
171	1	1	1818	gnl|PID|d102251	beta-galactosidase [Bacillus circulans]	74	62	1818
172	4	1064	2392	gi|466474	cellobiose phosphotransferase enzyme II'' [Bacillus stearothermophilus]	74	50	1329
185	1	326	3	gi|1573646	Mg(2+) transport ATPase protein C (mgtC) (SP:P22037) [Haemophilus influenzae]	74	68	324
188	2	1089	2018	gi|1573008	ATP dependent translocator homolog (msbA) [Haemophilus influenzae]	74	44	930
189	11	6491	7174	gi|1661199	sakacin A production response regulator [Streptococcus mutans]	74	60	684
210	2	520	1287	gi|2293207	(AF008220) YtmQ [Bacillus subtilis]	74	60	768
261	1	836	192	gi|666983	putative ATP binding subunit [Bacillus subtilis]	74	55	645
263	3	1619	3655	gi|663232	Similarity with S. cerevisiae hypothetical 137.7 kD protein in subtelomeric Y' repeat region [Saccharomyces cerevisiae]	74	42	2037
265	2	844	1227	gi|49272	Asparaginase [Bacillus licheniformis]	74	64	384
368	1	1	942	gi|603998	unknown [Saccharomyces cerevisiae]	74	39	942
7	16	13357	11921	gnl|PID|d101324	YqhX [Bacillus subtilis]	73	57	1437
17	10	5706	5449	gnl|PID|e305362	unnamed protein product [Streptococcus thermophilus]	73	47	258
31	2	522	244	gnl|PID|d100576	single strand DNA binding protein [Bacillus subtilis]	73	55	279
32	6	5667	6194	gnl|PID|d101315	YqfG [Bacillus subtilis]	73	58	528
34	15	10281	9790	gnl|PID|d102151	(AB001684) ORF42c [Chlorella vulgaris]	73	46	492

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

<table>
<tr><th>Contig ID</th><th>ORF ID</th><th>Start (nt)</th><th>Stop (nt)</th><th>match acession</th><th>match gene name</th><th>% sim</th><th>% ident</th><th>length (nt)</th></tr>
<tr><td>40</td><td>12</td><td>9876</td><td>9226</td><td>gi|1173517</td><td>riboflavin synthase alpha subunit [Actinobacillus pleuropneumoniae]</td><td>73</td><td>55</td><td>651</td></tr>
<tr><td>55</td><td>2</td><td>3592</td><td>839</td><td>gnl|PID|d101887</td><td>cation-transporting ATPase PacL [Synechocystis sp.]</td><td>73</td><td>60</td><td>2754</td></tr>
<tr><td>55</td><td>18</td><td>17494</td><td>16586</td><td>gnl|PID|e265580</td><td>unknown [Mycobacterium tuberculosis]</td><td>73</td><td>52</td><td>909</td></tr>
<tr><td>65</td><td>16</td><td>7213</td><td>7767</td><td>gi|143419</td><td>ribosomal protein L6 [Bacillus stearothermophilus]</td><td>73</td><td>60</td><td>555</td></tr>
<tr><td>66</td><td>3</td><td>3300</td><td>3659</td><td>gnl|PID|e269883</td><td>LacF [Lactobacillus casei]</td><td>73</td><td>52</td><td>360</td></tr>
<tr><td>70</td><td>10</td><td>5557</td><td>5733</td><td>gi|857631</td><td>envelope protein [Human immunodeficiency virus type 1]</td><td>73</td><td>60</td><td>177</td></tr>
<tr><td>71</td><td>4</td><td>6133</td><td>8262</td><td>gnl|PID|e322063</td><td>ss-1,4-galactosyltransferase [Streptococcus pneumoniae]</td><td>73</td><td>45</td><td>2130</td></tr>
<tr><td>72</td><td>1</td><td>3</td><td>851</td><td>gi|2293177</td><td>(AF008220) transporter [Bacillus subtilis]</td><td>73</td><td>50</td><td>849</td></tr>
<tr><td>76</td><td>7</td><td>7019</td><td>6195</td><td>gnl|PID|d101325</td><td>YqiF [Bacillus subtilis]</td><td>73</td><td>66</td><td>825</td></tr>
<tr><td>76</td><td>12</td><td>10009</td><td>9533</td><td>gi|1573086</td><td>uridine kinase (uridine monophosphokinase) (udk) [Haemophilus influenzae]</td><td>73</td><td>54</td><td>477</td></tr>
<tr><td>80</td><td>7</td><td>8113</td><td>9372</td><td>gi|1377823</td><td>aminopeptidase [Bacillus subtilis]</td><td>73</td><td>60</td><td>1260</td></tr>
<tr><td>97</td><td>5</td><td>3389</td><td>1668</td><td>gnl|PID|d101954</td><td>dihydroxyacid dehydratase [Synechocystis sp.]</td><td>73</td><td>54</td><td>1722</td></tr>
<tr><td>98</td><td>9</td><td>6912</td><td>7619</td><td>gnl|PID|e314991</td><td>FtsE [Mycobacterium tuberculosis]</td><td>73</td><td>54</td><td>708</td></tr>
<tr><td>108</td><td>11</td><td>10928</td><td>10440</td><td>gi|388109</td><td>regulatory protein [Enterococcus faecalis]</td><td>73</td><td>54</td><td>489</td></tr>
<tr><td>128</td><td>6</td><td>3632</td><td>4222</td><td>gi|1685111</td><td>orf1091 [Streptococcus thermophilus]</td><td>73</td><td>63</td><td>591</td></tr>
<tr><td>138</td><td>2</td><td>1575</td><td>394</td><td>gi|147326</td><td>transport protein [Escherichia coli]</td><td>73</td><td>60</td><td>1182</td></tr>
<tr><td>140</td><td>13</td><td>12538</td><td>11903</td><td>pir|E53402|E534</td><td>serine O-acetyltransferase (EC 2.3.1.30) - Bacillus stearothermophilus</td><td>73</td><td>55</td><td>636</td></tr>
<tr><td>162</td><td>5</td><td>5701</td><td>4991</td><td>gnl|PID|e323511</td><td>putative YhaQ protein [Bacillus subtilis]</td><td>73</td><td>50</td><td>711</td></tr>
<tr><td>164</td><td>4</td><td>2323</td><td>2790</td><td>gi|1592076</td><td>hypothetical protein (SP:P25768) [Methanococcus jannaschii]</td><td>73</td><td>52</td><td>468</td></tr>
<tr><td>164</td><td>8</td><td>4815</td><td>5546</td><td>gi|410137</td><td>ORFX13 [Bacillus subtilis]</td><td>73</td><td>56</td><td>732</td></tr>
<tr><td>170</td><td>5</td><td>4394</td><td>5302</td><td>gnl|PID|d100959</td><td>homologue of unidentified protein of E. coli [Bacillus subtilis]</td><td>73</td><td>46</td><td>909</td></tr>
<tr><td>178</td><td>7</td><td>3893</td><td>4855</td><td>gi|46242</td><td>nodulation protein B, 5'end [Rhizobium loti]</td><td>73</td><td>56</td><td>963</td></tr>
<tr><td>204</td><td>6</td><td>5096</td><td>4278</td><td>gnl|PID|e214719</td><td>PlcR protein [Bacillus thuringiensis]</td><td>73</td><td>41</td><td>819</td></tr>
<tr><td>213</td><td>2</td><td>832</td><td>2037</td><td>gi|1565296</td><td>ribosomal protein S1 homolog; sequence specific DNA-binding protein [Leuconostoc lactis]</td><td>73</td><td>55</td><td>1206</td></tr>
<tr><td>231</td><td>2</td><td>84</td><td>287</td><td>gi|40173</td><td>homolog of E.coli ribosomal protein L21 [Bacillus subtilis]</td><td>73</td><td>61</td><td>204</td></tr>
<tr><td>237</td><td>1</td><td>2</td><td>505</td><td>gi|1773151</td><td>adenine phosphoribosyltransferase [Escherichia coli]</td><td>73</td><td>51</td><td>504</td></tr>
</table>

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
269	1	2	691	gnl|PID|d101328	YqiX [Bacillus subtilis]	73	36	690
289	2	1272	832	pir|A02771|R7MC	ribosomal protein L7/L12 - Micrococcus luteus	73	66	441
343	1	14	484	gi|1788125	(AE000276) hypothetical 30.4 kD protein in manZ-cspC intergenic region [Escherichia coli]	73	47	471
356	1	222	4	gi|2149905	D-glutamic acid adding enzyme [Enterococcus faecalis]	73	50	219
7	5	3165	4691	gnl|PID|d101833	amidase [Synechocystis sp.]	72	52	1527
7	9	7195	7647	gi|146976	nusB [Escherichia coli]	72	54	453
7	17	13743	13300	gnl|PID|e289141	similar to hydroxymyristoyl-(acyl carrier protein) dehydratase [Bacillus subtilis]	72	59	444
22	19	15637	16224	gnl|PID|d101929	ribosome releasing factor [Synechocystis sp.]	72	51	588
33	17	12111	11425	gnl|PID|d101190	ORF3 [Streptococcus mutans]	72	55	687
34	7	7147	5627	gi|396501	aspartyl-tRNA synthetase [Thermus thermophilus]	72	52	1521
38	23	15372	16085	pir|H64108|H641	L-ribulose-phosphate 4-epimerase (araD) homolog - Haemophilus influenzae (strain Rd KW20)	72	54	714
39	5	5094	6905	gnl|PID|e254877	unknown [Mycobacterium tuberculosis]	72	56	1812
40	6	4469	4636	gi|153672	lactose repressor [Streptococcus mutans]	72	58	168
48	2	1459	1253	gi|310380	inhibin beta-A-subunit [Ovis aries]	72	33	207
48	29	21729	22424	gi|2314329	(AE000623) glutamine ABC transporter, permease protein (glnP) [Helicobacter pylori]	72	49	696
50	5	4529	3288	gi|1750108	YnbA [Bacillus subtilis]	72	54	1242
51	3	1044	2282	gi|2293230	(AF008220) YtbJ [Bacillus subtilis]	72	54	1239
52	13	13681	13938	gi|142521	deoxyribodipyrimidine photolyase [Bacillus subtilis]	72	45	258
55	1	841	35	gi|882518	ORF_o304; GTG start [Escherichia coli]	72	59	807
75	5	2832	3191	gnl|PID|e209886	mercuric resistance operon regulatory protein [Bacillus subtilis]	72	44	360
76	6	6229	5771	gi|142450	ahrC protein [Bacillus subtilis]	72	53	459
79	5	5065	4592	gi|2293279	(AF008220) YtcG [Bacillus subtilis]	72	46	474
87	14	14726	12309	gnl|PID|e323502	putative PriA protein [Bacillus subtilis]	72	52	2418
91	1	444	662	gi|500691	MYO1 gene product [Saccharomyces cerevisiae]	72	50	219
91	7	4516	4764	gi|829615	skeletal muscle sodium channel alpha-subunit [Equus caballus]	72	38	249

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
95	2	2004	1717	gnl|PID|e323527	putative Asp23 protein [Bacillus subtilis]	72	40	288
109	1	1452	118	gi|143331	alkaline phosphatase regulatory protein [Bacillus subtilis]	72	52	1335
126	1	3	2192	gnl|PID|d101831	glutamine-binding periplasmic protein [Synechocystis sp.]	72	46	2190
130	3	1735	2478	gi|2415396	(AF015775) carboxypeptidase [Bacillus subtilis]	72	53	744
137	6	2585	2929	gi|472922	v-type Na-ATPase [Enterococcus hirae]	72	46	345
140	10	9601	9203	gi|49224	URF 4 [Synechococcus sp.]	72	48	399
146	5	1906	1247	gnl|PID|e324945	hypothetical protein [Bacillus subtilis]	72	45	660
147	2	2084	1083	gnl|PID|e325016	hypothetical protein [Bacillus subtilis]	72	56	1002
147	5	6156	5146	gi|472327	TPP-dependent acetoin dehydrogenase beta-subunit [Clostridium magnum]	72	56	1011
148	8	5381	6433	gi|974332	NAD(P)H-dependent dihydroxyacetone-phosphate reductase [Bacillus subtilis]	72	54	1053
148	14	10256	9675	gnl|PID|d101319	YqgN [Bacillus subtilis]	72	50	582
159	8	4005	4949	gi|1788770	(AE000330) o463; 24 pct identical (44 gaps) to 338 residues from penicillin-binding protein 4*, PBPE_BACSU SW: P32959 (451 aa) [Escherichia coli]	72	43	945
172	10	9907	10620	gi|763387	unknown [Saccharomyces cerevisiae]	72	55	714
220	3	2862	3602	gi|1574175	hypothetical [Haemophilus influenzae]	72	50	741
267	1	3	449	gi|290513	f470 [Escherichia coli]	72	48	447
281	2	899	540	gnl|PID|d100964	homologue of aspartokinase 2 alpha and beta subunits LysC of B. subtilis [Bacillus subtilis]	72	45	360
290	1	1018	14	gi|474195	This ORF is homologous to a 40.0 kd hypothetical protein in the htrB 3' region from E. coli, Accession Number X61000 [Mycoplasma-like organism]	72	54	1005
300	1	63	587	gi|746399	transcription elongation factor [Escherichia coli]	72	50	525
316	1	1326	4	gi|158127	protein kinase C [Drosophila melanogaster]	72	40	1323
342	1	227	3	gnl|PID|d101164	unknown [Bacillus subtilis]	72	54	225
354	1	1	1005	gnl|PID|d102048	C. thermocellum beta-glucosidase; P26208 (985) [Bacillus subtilis]	72	52	1005
6	10	8134	10467	gnl|PID|e264229	unknown [Mycobacterium tuberculosis]	71	57	2334
7	20	16231	15464	gi|18046	3-oxoacyl-[acyl-carrier protein] reductase [Cuphea lanceolata]	71	52	768
15	1	1297	2	gnl|PID|d100571	replicative DNA helicase [Bacillus subtilis]	71	51	1296
15	4	4435	3869	gi|499384	orf189 [Bacillus subtilis]	71	47	567

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
18	6	5120	4218	gnl|PID|d101318	YqgG [Bacillus subtilis]	71	51	903
29	1	1	540	gi|1773142	similar to the 20.2kd protein in TETB-EXOA region of B. subtilis [Escherichia coli]	71	56	540
38	20	13327	13830	gi|537036	ORF_o158 [Escherichia coli]	71	48	504
51	12	15015	12676	gi|149528	dipeptidyl peptidase IV [Lactococcus lactis]	71	55	2340
55	23	21040	20585	gi|2343285	(AF015453) surface located protein [Lactobacillus rhamnosus]	71	58	456
60	2	705	265	gnl|PID|d101320	YqgZ [Bacillus subtilis]	71	44	441
71	18	24679	26226	gi|580920	rodD (gtaA) polypeptide (AA 1-673) [Bacillus subtilis]	71	44	1548
71	25	30587	30360	gi|606028	ORF_o414; Geneplot suggests frameshift near start but none found [Escherichia coli]	71	50	228
72	6	5239	6729	gi|580835	lysine decarboxylase [Bacillus subtilis]	71	48	1491
72	14	11991	12878	gi|624085	similar to rat beta-alanine synthetase encoded by GenBank Accession Number S27881; contains ATP/GTP binding motif [Paramecium bursaria Chlorella virus 1]	71	54	888
73	11	7269	7033	gi|1906594	PN1 [Rattus norvegicus]	71	42	237
74	6	10385	8517	gi|1573733	prolyl-tRNA synthetase (proS) [Haemophilus influenzae]	71	52	1869
81	9	5772	6578	gi|147404	mannose permease subunit II-M-Man [Escherichia coli]	71	45	807
86	5	4602	3604	gnl|PID|e322063	ss-1,4-galactosyltransferase [Streptococcus pneumoniae]	71	53	999
105	4	3619	4707	gi|2323341	(AF014460) PepQ [Streptococcus mutans]	71	58	1089
106	13	13557	12955	gi|1519287	LemA [Listeria monocytogenes]	71	48	603
114	2	1029	1979	gi|310303	mosA [Rhizobium meliloti]	71	55	951
122	2	564	1205	gi|1649037	glutamine transport ATP-binding protein GLNQ [Salmonella typhimurium]	71	50	642
132	5	9018	7063	gnl|PID|d102049	H. influenzae hypothetical ABC transporter; P44808 (974) [Bacillus subtilis]	71	51	1956
140	1	1141	227	gi|1673788	(AE000015) Mycoplasma pneumoniae, fructose-bisphosphate aldolase; similar to Swiss-Prot Accession Number P13243, from B. subtilis [Mycoplasma pneumoniae]	71	49	915
140	5	5635	4973	gnl|PID|d100964	homologue of hypothetical protein in a rapamycin synthesis gene cluster of Streptomyces hygroscopicus [Bacillus subtilis]	71	48	663
141	7	7369	7845	gnl|PID|d102005	(AB001488) FUNCTION UNKNOWN, SIMILAR PRODUCT IN E. COLI AND MYCOPLASMA PNEUMONIAE. [Bacillus subtilis]	71	51	477

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
193	1	1	165	gi|46912	ribosomal protein L13 [Staphylococcus carnosus]	71	59	165
194	3	2205	1594	gi|535351	CodY [Bacillus subtilis]	71	52	612
199	3	1510	1319	gi|2182574	(AE000090) Y4pE [Rhizobium sp. NGR234]	71	45	192
208	2	2616	3752	gi|1787378	(AE000213) hypothetical protein in purB 5' region [Escherichia coli]	71	57	1137
209	2	2022	1141	gi|41432	fepC gene product [Escherichia coli]	71	46	882
210	5	1911	3071	gi|49316	ORF2 gene product [Bacillus subtilis]	71	45	1161
210	6	3069	3386	gi|580900	ORF3 gene product [Bacillus subtilis]	71	48	318
212	2	3561	1381	gi|557567	ribonucleotide reductase R1 subunit [Mycobacterium tuberculosis]	71	53	2181
233	3	2003	2920	gnl|PID|d101320	YqgR [Bacillus subtilis]	71	50	918
244	1	13	1053	gnl|PID|d100964	homologue of aspartokinase 2 alpha and beta subunits LysC of B. subtilis [Bacillus subtilis]	71	55	1041
251	2	1008	1874	gi|755601	unknown [Bacillus subtilis]	71	46	867
282	2	906	712	gi|1353874	unknown [Rhodobacter capsulatus]	71	46	195
312	4	2137	1565	gnl|PID|d102245	(AB005554) yxbF [Bacillus subtilis]	71	34	573
338	1	3	683	gi|1591045	hypothetical protein (SP:P31466) [Methanococcus jannaschii]	71	48	681
346	1	3	164	gi|1591234	hypothetical protein (SP:P42297) [Methanococcus jannaschii]	71	36	162
374	1	619	2	gi|397526	clumping factor [Staphylococcus aureus]	71	23	618
377	1	688	2	gi|397526	clumping factor [Staphylococcus aureus]	71	23	687
3	8	7419	6958	gnl|PID|e269486	Unknown [Bacillus subtilis]	70	42	462
3	10	8395	9075	gnl|PID|e255543	putative iron dependant repressor [Staphylococcus epidermidis]	70	46	681
7	14	11024	10254	gnl|PID|d100290	undefined open reading frame [Bacillus stearothermophilus]	70	55	771
7	18	14213	13719	gnl|PID|d101090	biotin carboxyl carrier protein of acetyl-CoA carboxylase [Synechocystis sp.]	70	56	495
9	2	1057	287	gnl|PID|d100581	unknown [Bacillus subtilis]	70	52	771
12	4	2610	1789	gnl|PID|d101195	yycJ [Bacillus subtilis]	70	52	822
21	2	2586	1846	gi|2293447	(AF008930) ATPase [Bacillus subtilis]	70	54	741
22	13	10955	11512	gi|1165295	Ydr540cp [Saccharomyces cerevisiae]	70	50	558
30	6	4315	3980	gi|39478	ATP binding protein of transport ATPases [Bacillus firmus]	70	51	336

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
31	1	370	113	gi|662792	single-stranded DNA binding protein [unidentified eubacterium]	70	36	258
33	15	10639	9521	gi|1161219	homolgous to D-amino acid dehydrogenase enzyme [Pseudomonas aeruginosa]	70	50	1119
38	6	3812	4312	gi|2058547	ComYD [Streptococcus gordonii]	70	48	501
38	25	17986	18477	gi|537033	ORF_f356 [Escherichia coli]	70	58	492
40	13	11054	9846	gi|1173516	riboflavin-specific deaminase [Actinobacillus pleuropneumoniae]	70	52	1209
42	2	722	1954	gi|1146183	putative [Bacillus subtilis]	70	51	1233
43	3	2373	1612	gi|1591493	glutamine transport ATP-binding protein Q [Methanococcus jannaschii]	70	48	762
45	8	9197	8049	gnl|PID|d102036	subunit of ADP-glucose pyrophosphorylase [Bacillus stearothermophilus]	70	54	1149
59	2	567	956	gnl|PID|d100302	neopullulanase [Bacillus sp.]	70	42	390
60	3	1874	795	gnl|PID|e276466	aminopeptidase P [Lactococcus lactis]	70	48	1080
61	4	5553	2437	gnl|PID|e275074	SNF [Bacillus cereus]	70	51	3117
61	7	7914	6802	gi|1573037	cystathionine gamma-synthase (metB) [Haemophilus influenzae]	70	52	1113
63	7	5372	7222	gnl|PID|d100974	unknown [Bacillus subtilis]	70	54	1851
68	7	7126	6962	gi|1263014	emm18.1 gene product [Streptococcus pyogenes]	70	37	165
72	12	10081	10911	gi|2313093	(AE000524) carboxynorspermidine decarboxylase (nspC) [Helicobacter pylori]	70	56	831
75	10	7888	8124	gi|1877423	galactose-1-P-uridyl transferase [Streptococcus mutans]	70	59	237
79	3	3424	2525	gi|39881	ORF 311 (AA 1-311) [Bacillus subtilis]	70	47	900
87	10	9369	7324	gnl|PID|e323506	putative Pkn2 protein [Bacillus subtilis]	70	52	2046
96	14	10640	11788	gi|1573209	tRNA-guanine transglycosylase (tgt) [Haemophilus influenzae]	70	52	1149
113	2	574	1086	gi|433630	A180 [Saccharomyces cerevisiae]	70	59	513
123	5	2901	3461	gnl|PID|d100585	unknown [Bacillus subtilis]	70	45	561
125	5	4593	4282	gnl|PID|e276474	capacitative calcium entry channel 1 [Bos taurus]	70	35	312
129	5	4500	3454	gnl|PID|d101314	YqeT [Bacillus subtilis]	70	47	1047
133	3	2608	1394	gi|2293312	(AF008220) YtfP [Bacillus subtilis]	70	50	1215
135	1	420	662	gnl|PID|e265530	yorfE [Streptococcus pneumoniae]	70	47	243
137	3	438	932	gi|472919	v-type Na-ATPase [Enterococcus hirae]	70	57	495
138	1	440	3	gi|147336	transmembrane protein [Escherichia coli]	70	42	438

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
140	16	18796	16364	gi|976441	N5-methyltetrahydrofolate homocysteine methyltransferase [Saccharomyces cerevisiae]	70	53	2433
167	10	8263	6695	gi|149535	D-alanine activating enzyme [Lactobacillus casei]	70	52	1569
204	4	3226	2747	gnl|PID|d102049	E. coli hypothetical protein; P31805 (267) [Bacillus subtilis]	70	51	480
207	3	2627	2869	gnl|PID|e309213	racGAP [Dictyostelium discoideum]	70	45	243
282	3	1136	882	gi|1353874	unknown [Rhodobacter capsulatus]	70	50	255
6	21	17554	18453	gnl|PID|e233879	hypothetical protein [Bacillus subtilis]	69	44	900
6	22	18482	19471	gi|580883	ipa-88d gene product [Bacillus subtilis]	69	53	990
22	6	4682	5824	gi|2209379	(AF006720) ProJ [Bacillus subtilis]	69	48	1143
22	9	7992	8651	gnl|PID|d100580	unknown [Bacillus subtilis]	69	51	660
22	12	9871	10767	gnl|PID|d100581	unknown [Bacillus subtilis]	69	51	897
27	7	5857	5348	gnl|PID|d102012	(AB001488) FUNCTION UNKNOWN. [Bacillus subtilis]	69	28	510
36	10	7294	10116	gi|437916	isoleucyl-tRNA synthetase [Staphylococcus aureus]	69	53	2823
38	1	2	1090	gi|141900	alcohol dehydrogenase (EC 1.1.1.1) [Alcaligenes eutrophus]	69	48	1089
40	14	11333	11944	gi|1573280	Holliday junction DNA helicase (ruvA) [Haemophilus influenzae]	69	44	612
40	15	11942	12517	gi|1573653	DNA-3-methyladenine glycosidase I (tagI) [Haemophilus influenzae]	69	50	576
45	6	6947	5490	gi|580887	starch (bacterial glycogen) synthase [Bacillus subtilis]	69	47	1458
48	34	24932	24153	gnl|PID|e233870	hypothetical protein [Bacillus subtilis]	69	36	780
49	6	6183	6521	gi|396297	similar to phosphotransferase system enzyme II [Escherichia coli]	69	50	339
49	8	7586	8338	gi|396420	similar to Alcaligenes eutrophus pHG1 D-ribulose-5-phosphate 3 epimerase [Escherichia coli]	69	49	753
55	6	8262	7033	gi|1146238	poly(A) polymerase [Bacillus subtilis]	69	50	1230
59	3	954	2333	gnl|PID|e313038	hypothetical protein [Bacillus subtilis]	69	54	1380
62	3	1170	1418	gnl|PID|d101915	hypothetical protein [Synechocystis sp.]	69	49	249
63	8	7298	7762	gi|293017	ORF3 (put.); putative [Lactococcus lactis]	69	42	465
66	4	3657	5081	gi|153755	phospho-beta-D-galactosidase (EC 3.2.1.85) [Lactococcus lactis cremoris]	69	49	1425
66	5	5126	6829	gi|433809	enzyme II [Streptococcus mutans]	69	46	1704
71	6	10017	10664	gnl|PID|e322063	ss-1,4-galactosyltransferase [Streptococcus pneumoniae]	69	39	648

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
71	21	27730	27966	gnl|PID|d100649	DE-cadherin [Drosophila melanogaster]	69	30	237
77	1	1	237	gi|287870	groES gene product [Lactococcus lactis]	69	44	237
81	5	3622	4101	gi|1573605	fucose operon protein (fucU) [Haemophilus influenzae]	69	52	480
83	1	40	714	pir|C33496|C334	hisC homolog - Bacillus subtilis	69	46	675
83	16	15742	16335	gi|143372	phosphoribosyl glycinamide formyltransferase (PUR-N) [Bacillus subtilis]	69	46	594
85	2	1212	916	gi|194097	IFN-response element binding factor 1 [Mus musculus]	69	48	297
91	5	3678	4274	gi|1574712	anaerobic ribonuleoside-triphosphate reductase activating protein (nrdG) [Haemophilus influenzae]	69	44	597
98	5	3247	4032	gnl|PID|d100262	LivF protein [Salmonella typhimurium]	69	51	786
108	5	4085	5056	gnl|PID|e257629	transcription factor [Lactococcus lactis]	69	49	972
126	3	3078	4568	gnl|PID|d101329	YqjJ [Bacillus subtilis]	69	49	1491
131	6	4121	2889	gnl|PID|d101314	YqeR [Bacillus subtilis]	69	47	1233
136	2	1505	2299	gnl|PID|d100581	unknown [Bacillus subtilis]	69	47	795
149	5	3852	4763	gnl|PID|e323525	YloQ protein [Bacillus subtilis]	69	50	912
149	12	9336	10655	gi|151571	Homology with E.coli and P.aeruginosa lysA gene; product of unknown function; putative [Pseudomonas syringae]	69	52	1320
153	4	3191	3829	gi|1710373	BrnQ [Bacillus subtilis]	69	44	639
169	3	849	2324	gnl|PID|d100582	temperature sensitive cell division [Bacillus subtilis]	69	49	1476
180	1	566	3	gi|488339	alpha-amylase [unidentified cloning vector]	69	50	564
212	1	1196	231	gi|1395209	ribonucleotide reductase R2-2 small subunit [Mycobacterium tuberculosis]	69	53	966
226	1	2	661	pir|JQ2285|JQ22	nodulin-26 - soybean	69	41	660
233	5	3249	4766	gi|472918	v-type Na-ATPase [Enterococcus hirae]	69	56	1518
235	3	660	1766	gi|148945	methylase [Haemophilus influenzae]	69	43	1107
243	2	865	2361	gnl|PID|d100225	ORF5 [Barley yellow dwarf virus]	69	69	1497
251	3	2899	1967	gi|2289231	macrolide-efflux protein [Streptococcus agalactiae]	69	51	933
310	1	1	282	gnl|PID|e322442	peptide deformylase [Clostridium beijerinckii]	69	55	282
369	1	868	2	gi|397526	clumping factor [Staphylococcus aureus]	69	22	867
370	1	749	3	gi|397526	clumping factor [Staphylococcus aureus]	69	21	747

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

<table>
<tr><th>Contig ID</th><th>ORF ID</th><th>Start (nt)</th><th>Stop (nt)</th><th>match acession</th><th>match gene name</th><th>% sim</th><th>% ident</th><th>length (nt)</th></tr>
<tr><td>379</td><td>1</td><td>44</td><td>280</td><td>gnl|PID|d100649</td><td>DE-cadherin [Drosophila melanogaster]</td><td>69</td><td>30</td><td>237</td></tr>
<tr><td>388</td><td>1</td><td>260</td><td>72</td><td>gi|1787524</td><td>(AE000225) hypothetical 32.7 kD protein in trpL-btuR intergenic region [Escherichia coli]</td><td>69</td><td>44</td><td>189</td></tr>
<tr><td>1</td><td>2</td><td>2006</td><td>3040</td><td>gnl|PID|d101809</td><td>ABC transporter [Synechocystis sp.]</td><td>68</td><td>43</td><td>1035</td></tr>
<tr><td>12</td><td>5</td><td>3958</td><td>2600</td><td>gi|2182992</td><td>histidine kinase [Lactococcus lactis cremoris]</td><td>68</td><td>45</td><td>1359</td></tr>
<tr><td>15</td><td>2</td><td>1790</td><td>1311</td><td>pir|S16974|R5BS</td><td>ribosomal protein L9 - Bacillus stearothermophilus</td><td>68</td><td>56</td><td>480</td></tr>
<tr><td>16</td><td>6</td><td>7353</td><td>5701</td><td>gi|1787041</td><td>(AE000184) o530; This 530 aa orf is 33 pct identical (14 gaps) to 525 residues of an approx. 640 aa protein YHES_HAEIN SW: P44808 [Escherichia coli]</td><td>68</td><td>45</td><td>1653</td></tr>
<tr><td>17</td><td>12</td><td>6479</td><td>6805</td><td>gi|553165</td><td>acetylcholinesterase [Homo sapiens]</td><td>68</td><td>68</td><td>327</td></tr>
<tr><td>20</td><td>13</td><td>14128</td><td>14505</td><td>gi|142700</td><td>P competence protein (ttg start codon) (put.); putative [Bacillus subtilis]</td><td>68</td><td>40</td><td>378</td></tr>
<tr><td>22</td><td>32</td><td>24612</td><td>25397</td><td>gi|289262</td><td>comE ORF3 [Bacillus subtilis]</td><td>68</td><td>36</td><td>786</td></tr>
<tr><td>30</td><td>7</td><td>4548</td><td>4288</td><td>gi|311388</td><td>ORF1 [Azorhizobium caulinodans]</td><td>68</td><td>46</td><td>261</td></tr>
<tr><td>36</td><td>5</td><td>3911</td><td>4585</td><td>gi|1573041</td><td>hypothetical [Haemophilus influenzae]</td><td>68</td><td>54</td><td>675</td></tr>
<tr><td>46</td><td>6</td><td>5219</td><td>6040</td><td>gi|1790131</td><td>(AE000446) hypothetical 29.7 kD protein in ibpA-gyrB intergenic region [Escherichia coli]</td><td>68</td><td>47</td><td>822</td></tr>
<tr><td>54</td><td>10</td><td>6235</td><td>7086</td><td>gi|882579</td><td>CG Site No. 29739 [Escherichia coli]</td><td>68</td><td>55</td><td>852</td></tr>
<tr><td>55</td><td>5</td><td>7069</td><td>5165</td><td>gnl|PID|d101914</td><td>ABC transporter [Synechocystis sp.]</td><td>68</td><td>45</td><td>1905</td></tr>
<tr><td>71</td><td>3</td><td>6134</td><td>5613</td><td>gi|1573353</td><td>outer membrane integrity protein (tolA) [Haemophilus influenzae]</td><td>68</td><td>50</td><td>522</td></tr>
<tr><td>71</td><td>10</td><td>15342</td><td>16613</td><td>gi|580866</td><td>ipa-12d gene product [Bacillus subtilis]</td><td>68</td><td>31</td><td>1272</td></tr>
<tr><td>71</td><td>12</td><td>17560</td><td>18792</td><td>gi|44073</td><td>SecY protein [Lactococcus lactis]</td><td>68</td><td>35</td><td>1233</td></tr>
<tr><td>71</td><td>17</td><td>22295</td><td>24703</td><td>gi|1762349</td><td>involved in protein export [Bacillus subtilis]</td><td>68</td><td>50</td><td>2409</td></tr>
<tr><td>73</td><td>16</td><td>10208</td><td>9729</td><td>gi|1353537</td><td>dUTPase [Bacteriophage r1t]</td><td>68</td><td>51</td><td>480</td></tr>
<tr><td>86</td><td>18</td><td>17198</td><td>16011</td><td>gi|413943</td><td>ipa-19d gene product [Bacillus subtilis]</td><td>68</td><td>53</td><td>1188</td></tr>
<tr><td>87</td><td>17</td><td>17491</td><td>15866</td><td>gi|150209</td><td>ORF 1 [Mycoplasma mycoides]</td><td>68</td><td>43</td><td>1626</td></tr>
<tr><td>89</td><td>6</td><td>5139</td><td>4354</td><td>gi|1498824</td><td>M. jannaschii predicted coding region MJ0062 [Methanococcus jannaschii]</td><td>68</td><td>40</td><td>786</td></tr>
<tr><td>89</td><td>11</td><td>8021</td><td>8242</td><td>gi|150974</td><td>4-oxalocrotonate tautomerase [Pseudomonas putida]</td><td>68</td><td>43</td><td>222</td></tr>
<tr><td>97</td><td>8</td><td>6755</td><td>5394</td><td>gi|2367358</td><td>(AE000491) hypothetical 52.9 kD protein in aidB-rpsF intergenic region [Escherichia coli]</td><td>68</td><td>41</td><td>1362</td></tr>
</table>

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
98	3	1418	2308	gnl|PID|d100261	LivA protein [Salmonella typhimurium]	68	40	891
99	13	16414	17280	gi|455363	regulatory protein [Streptococcus mutans]	68	50	867
115	3	5054	3693	gi|466474	cellobiose phosphotransferase enzyme II'' [Bacillus stearothermophilus]	68	44	1362
124	7	3394	3221	gnl|PID|d100702	cut14 protein [Schizosaccharomyces pombe]	68	56	174
125	2	2923	1922	gi|450566	transmembrane protein [Bacillus subtilis]	68	50	1002
132	2	4858	2888	gnl|PID|d101732	DNA ligase [Synechocystis sp.]	68	52	1971
140	7	7765	7580	gi|1209711	unknown [Saccharomyces cerevisiae]	68	47	186
150	1	539	3	gi|402490	ADP-ribosylarginine hydrolase [Mus musculus]	68	59	537
164	1	58	867	gnl|PID|e255114	glutamate racemase [Bacillus subtilis]	68	49	810
164	2	819	1835	gnl|PID|e255117	hypothetical protein [Bacillus subtilis]	68	50	1017
169	7	3946	4104	pir|B54545|B545	hypothetical protein - Lactococcus lactis subsp. lactis plasmid pSL2	68	40	159
170	4	4247	4396	gi|304146	spore coat protein [Bacillus subtilis]	68	52	150
171	8	6002	7054	gi|38722	precursor (aa -20 to 381) [Acinetobacter calcoaceticus]	68	54	1053
198	3	2473	1871	gnl|PID|e313075	hypothetical protein [Bacillus subtilis]	68	46	603
211	2	969	1802	gi|1439528	EIIC-man [Lactobacillus curvatus]	68	45	834
214	8	4926	4231	gnl|PID|d102049	H. influenzae hypothetical protein; P43990 (182) [Bacillus subtilis]	68	50	696
217	6	4955	5170	gnl|PID|e326966	similar to B.vulgaris CMS-associated mitochondrial ... (reverse transcriptase) [Arabidopsis thaliana]	68	36	216
218	7	3930	4745	gi|2293198	(AF008220) YtgP [Bacillus subtilis]	68	38	816
220	6	4628	4338	gnl|PID|e325791	(AJ000005) orf1 [Bacillus megaterium]	68	51	291
236	1	746	108	gi|410137	ORFX13 [Bacillus subtilis]	68	46	639
237	2	675	1451	gi|396348	homoserine transsuccinylase [Escherichia coli]	68	49	777
250	4	771	1229	gi|310859	ORF2 [Synechococcus sp.]	68	50	459
254	1	517	155	gi|1787105	(AE000189) o648 was o669; This 669 aa orf is 40 pct identical (1 gaps) to 217 residues of an approx. 232 aa protein YBBA_HAEIN SW: P45247 [Escherichia coli]	68	44	363
337	1	1	774	gnl|PID|e261990	putative orf [Bacillus subtilis]	68	47	774
345	1	3	653	gi|149513	thymidylate synthase (EC 2.1.1.45) [Lactococcus lactis]	68	61	651

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
386	2	417	4	gi|1573353	outer membrane integrity protein (tolA) [Haemophilus influenzae]	68	51	414
2	4	5722	4697	gi|1592141	M. jannaschii predicted coding region MJ1507 [Methanococcus jannaschii]	67	26	1026
3	6	5397	4591	gi|2293175	(AF008220) signal transduction regulator [Bacillus subtilis]	67	44	807
5	2	2301	574	gi|2313385	(AE000547) para-aminobenzoate synthetase (pabB) [Helicobacter pylori]	67	48	1728
6	19	16063	16758	gi|413931	ipa-7d gene product [Bacillus subtilis]	67	41	696
22	8	7094	7897	gi|1928962	pyrroline-5-carboxylate reductase [Actinidia deliciosa]	67	51	804
29	10	8335	9072	gi|468745	gtcR gene product [Bacillus brevis]	67	41	738
31	3	1379	585	gi|2425123	(AF019986) PksB [Dictyostelium discoideum]	67	49	795
32	11	8849	10150	gi|42029	ORF1 gene product [Escherichia coli]	67	47	1302
36	16	14830	15546	gi|1592142	ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]	67	43	717
38	9	4958	5392	gnl|PID|e214803	T22B3.3 [Caenorhabditis elegans]	67	47	435
38	21	13775	14512	gi|537037	ORF_o216 [Escherichia coli]	67	52	738
45	9	10428	9181	gi|551710	branching enzyme (glgB) (EC 2.4.1.18) [Bacillus stearothermophilus]	67	51	1248
48	23	18344	17514	gi|413949	ipa-25d gene product [Bacillus subtilis]	67	50	831
50	2	1773	952	gnl|PID|d101330	YqjQ [Bacillus subtilis]	67	55	822
53	1	431	3	gi|1574291	fimbrial transcription regulation repressor (pilB) [Haemophilus influenzae]	67	40	429
55	13	12740	11946	gnl|PID|e252990	ORF YDL037c [Saccharomyces cerevisiae]	67	51	795
61	9	9210	8329	gnl|PID|e264711	ATP-binding cassette transporter A [Staphylococcus aureus]	67	50	882
71	2	5614	6117	gi|1197667	vitellogenin [Anolis pulchellus]	67	36	504
81	7	4489	4983	gi|1142714	phosphoenolpyruvate:mannose phosphotransferase element IIB [Lactobacillus curvatus]	67	42	495
83	7	2957	3214	gi|1276746	Acyl carrier protein [Porphyra purpurea]	67	37	258
86	8	8140	6809	gi|1147744	PSR [Enterococcus hirae]	67	45	1332
97	3	986	1366	gnl|PID|d102235	(AB000631) unnamed protein product [Streptococcus mutans]	67	43	381
102	1	601	1413	gi|682765	mccB gene product [Escherichia coli]	67	36	813
106	3	1109	1987	gi|148921	LicD protein [Haemophilus influenzae]	67	43	879
115	4	5982	5656	gi|895750	putative cellobiose phosphotransferase enzyme III [Bacillus subtilis]	67	44	327

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
115	7	8421	8077	gi|466473	cellobiose phosphotransferase enzyme II' [Bacillus stearothermophilus]	67	51	345
127	13	8127	7021	gi|147326	transport protein [Escherichia coli]	67	45	1107
136	3	2215	2859	gnl|PID|d100581	unknown [Bacillus subtilis]	67	49	645
140	21	23317	20906	gnl|PID|d101912	phenylalanyl-tRNA synthetase [Synechocystis sp.]	67	43	2412
146	6	2894	1893	gi|2182994	histidine kinase [Lactococcus lactis cremoris]	67	44	1002
151	8	11476	11117	gnl|PID|d100085	ORF129 [Bacillus cereus]	67	48	360
160	10	7453	8646	gi|2281317	OrfB; similar to a Streptococcus pneumoniae putative membrane protein encoded by GenBank Accession Number X99400; inactivation of the OrfB gene leads to UV-sensitivity and to decrease of homologous recombination (plasmidic test) [Lactococcus l	67	46	1194
163	3	3099	4505	gnl|PID|d101317	YqfR [Bacillus subtilis]	67	47	1407
167	8	6704	5454	gi|1161933	DltB [Lactobacillus casei]	67	45	1251
169	4	2322	2879	gnl|PID|d101331	YqkG [Bacillus subtilis]	67	41	558
171	11	7656	8384	gi|153841	pneumococcal surface protein A [Streptococcus pneumoniae]	67	50	729
188	3	1930	3723	gi|1542975	AbcB [Thermoanaerobacterium thermosulfurigenes]	67	46	1794
189	6	3599	3141	gnl|PID|e325178	Hypothetical protein [Bacillus subtilis]	67	52	459
205	3	1663	2211	gi|606073	ORF_o169 [Escherichia coli]	67	47	549
207	4	2896	3456	gi|2276374	DtxR/iron regulated lipoprotein precursor [Corynebacterium diphtheriae]	67	49	561
217	3	4086	3703	gi|895750	putative cellobiose phosphotransferase enzyme III [Bacillus subtilis]	67	42	384
246	2	291	662	gi|1842438	unknown [Bacillus subtilis]	67	43	372
252	1	2	745	gi|2351768	PspA [Streptococcus pneumoniae]	67	41	744
265	3	1134	1811	gi|2313847	(AE000585) L-asparaginase II (ansB) [Helicobacter pylori]	67	42	678
295	1	1	375	gi|2276374	DtxR/iron regulated lipoprotein precursor [Corynebacterium diphtheriae]	67	43	375
1	7	4898	5146	gnl|PID|e255179	unknown [Mycobacterium tuberculosis]	66	56	249
3	1	389	3	gnl|PID|e269548	Unknown [Bacillus subtilis]	66	48	387
3	20	19267	20805	gi|39956	IIGlc [Bacillus subtilis]	66	50	1539
4	3	2545	2718	gi|1787564	(AE000228) phage shock protein C [Escherichia coli]	66	36	174
5	9	13197	12592	gi|1574291	fimbrial transcription regulation repressor (pilB) [Haemophilus influenzae]	66	46	606

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
9	4	2872	1451	gnl|PID|e266928	unknown [Mycobacterium tuberculosis]	66	43	1422
12	2	1469	1200	gi|520407	orf2; GTG start codon [Bacillus thuringiensis]	66	42	270
15	12	10979	9897	gi|2314738	(AE000653) translation elongation factor EF-Ts (tsf) [Helicobacter pylori]	66	49	1083
16	2	1312	734	gnl|PID|d102245	(AB005554) yxbF [Bacillus subtilis]	66	35	579
22	3	1372	1851	gi|1480916	signal peptidase type II [Lactococcus lactis]	66	38	480
22	7	5828	7096	gnl|PID|e206261	gamma-glutamyl phosphate reductase [Streptococcus thermophilus]	66	51	1269
22	20	16194	17138	gnl|PID|e281914	YitL [Bacillus subtilis]	66	50	945
30	2	530	976	gi|2314379	(AE000627) ABC transporter, ATP-binding protein (yhcG) [Helicobacter pylori]	66	40	447
32	1	199	984	gi|312444	ORF2 [Bacillus caldolyticus]	66	49	786
33	13	8352	7234	gi|1387979	44% identity over 302 residues with hypothetical protein from Synechocystis sp, accession D64006_CD; expression induced by environmental stress; some similarity to glycosyl transferases; two potential membrane-spanning helices [Bacillus subtil	66	44	1119
34	6	5658	4708	gnl|PID|e250724	orf2 [Lactobacillus sake]	66	39	951
34	14	9792	9574	gi|1590997	M. jannaschii predicted coding region MJ0272 [Methanococcus jannaschii]	66	48	219
35	16	15163	14501	gi|1773352	Cap5M [Staphylococcus aureus]	66	46	663
36	9	6173	6976	gi|1518680	minicell-associated protein DivIVA [Bacillus subtilis]	66	35	804
36	11	10396	10824	bbs|155344	insulin activator factor, INSAF [human, Pancreatic insulinoma, Peptide Partial, 744 aa] [Homo sapiens]	66	43	429
48	1	28	1419	gnl|PID|e325204	hypothetical protein [Bacillus subtilis]	66	50	1392
48	7	3810	4112	gi|2182574	(AE000090) Y4pE [Rhizobium sp. NGR234]	66	40	303
52	4	3595	2789	gi|388565	major cell-binding factor [Campylobacter jejuni]	66	52	807
54	3	2662	1076	gnl|PID|d101831	glutamine-binding periplasmic protein [Synechocystis sp.]	66	43	1587
61	10	9740	9183	gnl|PID|e154144	mdr gene product [Staphylococcus aureus]	66	44	558
72	13	10893	11993	gi|2313129	(AE000526) H. pylori predicted coding region HP0049 [Helicobacter pylori]	66	44	1101
74	9	13267	12476	gi|1573941	hypothetical [Haemophilus influenzae]	66	43	792
75	1	2	868	gi|1574631	nicotinamide mononucleotide transporter (pnuC) [Haemophilus influenzae]	66	48	867
75	7	5303	4275	gi|41312	put. EBG repressor protein [Escherichia coli]	66	40	1029

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
82	7	6813	8123	gnl|PID|e255128	trigger factor [Bacillus subtilis]	66	53	1311
83	3	905	1219	pir|C33496|C334	hisC homolog - Bacillus subtilis	66	44	315
86	10	9407	8925	gi|683584	shikimate kinase [Lactococcus lactis]	66	41	483
88	10	7001	6060	gi|2098719	putative fimbrial-associated protein [Actinomyces naeslundii]	66	52	942
89	1	951	4	gi|410118	ORFX19 [Bacillus subtilis]	66	41	948
93	7	3661	2711	gi|1787936	(AE000260) f298; This 298 aa orf is 51 pct identical (5 gaps) to 297 residues of an approx. 304 aa protein YCSN_BACSU SW: P42972 [Escherichia coli]	66	49	951
104	3	1805	3049	gi|1469784	putative cell division protein ftsW [Enterococcus hirae]	66	48	1245
106	14	13576	14253	gi|40027	homologous to E.coli gidB [Bacillus subtilis]	66	52	678
107	3	965	1864	gi|144858	ORF A [Clostridium perfringens]	66	49	900
112	7	5718	6593	gi|609332	DprA [Haemophilus influenzae]	66	43	876
115	1	3	302	gi|727367	Hyr1p [Saccharomyces cerevisiae]	66	56	300
122	1	3	566	gnl|PID|d101328	YqiY [Bacillus subtilis]	66	36	564
126	8	11759	11046	gnl|PID|d101163	ORF3 [Bacillus subtilis]	66	48	714
128	11	8201	8431	gi|726288	growth associated protein GAP-43 [Xenopus laevis]	66	41	231
131	8	4894	4508	gi|486661	TMnm related protein [Saccharomyces cerevisiae]	66	39	387
140	3	3236	2574	gi|40056	phoP gene product [Bacillus subtilis]	66	36	663
140	15	16318	15434	gi|1658189	5,10-methylenetetrahydrofolate reductase [Erwinia carotovora]	66	48	885
146	12	7926	7636	gnl|PID|d101140	transposase [Synechocystis sp.]	66	42	291
147	6	7137	6154	gi|472326	TPP-dependent acetoin dehydrogenase alpha-subunit [Clostridium magnum]	66	48	984
149	6	4435	5430	gnl|PID|d101887	pentose-5-phosphate-3-epimerase [Synechocystis sp.]	66	46	996
149	13	10754	11575	gi|42371	pyruvate formate-lyase activating enzyme (AA 1-246) [Escherichia coli]	66	42	822
186	4	2578	2270	gnl|PID|d101199	ORF11 [Enterococcus faecalis]	66	41	309
207	2	2340	2597	gnl|PID|e321893	envelope glycoprotein gp160 [Human immunodeficiency virus type 1]	66	46	258
210	7	3358	3678	gi|49318	ORF4 gene product [Bacillus subtilis]	66	46	321
217	8	5143	5355	gi|49538	thrombin receptor [Cricetulus longicaudatus]	66	38	213
220	4	3875	3642	gi|466648	alternate name ORFD of L23635 [Escherichia coli]	66	33	234

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
223	1	1070	138	gnl|PID|e247187	zinc finger protein [Bacteriophage phigle]	66	45	933
224	2	1864	2640	gi|1176399	putative ABC transporter subunit [Staphylococcus epidermidis]	66	41	777
243	1	3	872	dbj||AB000617_2	(AB000617) YcdH [Bacillus subtilis]	66	45	870
268	2	891	568	gi|517210	putative transposase [Streptococcus pyogenes]	66	60	324
322	1	2	643	gi|1499836	Zn protease [Methanococcus jannaschii]	66	40	642
5	10	13909	13178	gi|1574292	hypothetical [Haemophilus influenzae]	65	34	732
6	11	10465	11190	gi|142854	homologous to E. coli radC gene product and to unidentified protein from Staphylococcus aureus [Bacillus subtilis]	65	48	726
7	2	647	405	pir|C64146|C641	hypothetical protein HI0259 - Haemophilus influenzae (strain Rd KW20)	65	42	243
7	7	6246	6821	gnl|PID|d101323	YqhU [Bacillus subtilis]	65	50	576
10	2	1873	1397	gi|1163111	ORF-1 [Streptococcus pneumoniae]	65	54	477
16	3	1428	2222	gnl|PID|e325010	hypothetical protein [Bacillus subtilis]	65	45	795
21	4	3815	3357	gnl|PID|e314910	hypothetical protein [Staphylococcus sciuri]	65	40	459
22	34	25776	26384	gi|1123030	CpxA [Actinobacillus pleuropneumoniae]	65	42	609
43	2	1648	290	gi|1044826	F14E5.1 [Caenorhabditis elegans]	65	38	1359
48	13	10062	10856	gi|1573390	hypothetical [Haemophilus influenzae]	65	45	795
48	22	17521	16883	gi|1573391	hypothetical [Haemophilus influenzae]	65	37	639
48	25	19027	18533	gnl|PID|e264484	YCR020c, len:215 [Saccharomyces cerevisiae]	65	38	495
49	3	3856	5334	gi|1480429	putative transcriptional regulator [Bacillus stearothermophilus]	65	32	1479
50	6	5337	4519	gi|171963	tRNA isopentenyl transferase [Saccharomyces cerevisiae]	65	42	819
52	15	14728	15588	gi|1499745	M. jannaschii predicted coding region MJ0912 [Methanococcus jannaschii]	65	46	861
59	7	3963	4745	gi|496514	orf zeta [Streptococcus pyogenes]	65	42	783
68	3	2500	3483	gi|887824	ORF_o310 [Escherichia coli]	65	46	984
69	3	2171	1077	gnl|PID|e311453	unknown [Bacillus subtilis]	65	42	1095
69	7	6029	5325	gi|809660	deoxyribose-phosphate aldolase [Bacillus subtilis]	65	55	705
71	5	8536	9783	gi|1573224	glycosyl transferase lgtC (GP:U14554_4) [Haemophilus influenzae]	65	42	1248
72	8	7664	8527	gnl|PID|e267589	Unknown, highly similar to several spermidine synthases [Bacillus subtilis]	65	39	864

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

<table>
<tr><th>Contig ID</th><th>ORF ID</th><th>Start (nt)</th><th>Stop (nt)</th><th>match acession</th><th>match gene name</th><th>% sim</th><th>% ident</th><th>length (nt)</th></tr>
<tr><td>76</td><td>5</td><td>5773</td><td>4097</td><td>gnl|PID|d101723</td><td>DNA REPAIR PROTEIN RECN (RECOMBINATION PROTEIN N). [Escherichia coli]</td><td>65</td><td>44</td><td>1677</td></tr>
<tr><td>76</td><td>9</td><td>8099</td><td>7875</td><td>gi|1574276</td><td>exodeoxyribonuclease, small subunit (xseB) [Haemophilus influenzae]</td><td>65</td><td>38</td><td>225</td></tr>
<tr><td>84</td><td>2</td><td>2870</td><td>2352</td><td>gi|2313188</td><td>(AE000532) conserved hypothetical protein [Helicobacter pylori]</td><td>65</td><td>41</td><td>519</td></tr>
<tr><td>86</td><td>15</td><td>14495</td><td>13407</td><td>gnl|PID|d101880</td><td>3-dehydroquinate synthase [Synechocystis sp.]</td><td>65</td><td>44</td><td>1089</td></tr>
<tr><td>87</td><td>3</td><td>3706</td><td>2423</td><td>gi|151259</td><td>HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii]</td><td>65</td><td>51</td><td>1284</td></tr>
<tr><td>88</td><td>3</td><td>2425</td><td>2736</td><td>gi|1098510</td><td>unknown [Lactococcus lactis]</td><td>65</td><td>30</td><td>312</td></tr>
<tr><td>89</td><td>2</td><td>1627</td><td>1007</td><td>gnl|PID|d102008</td><td>(AB001488) SIMILAR TO ORF14 OF ENTEROCOCCUS FAECALIS TRANSPOSON TN916. [Bacillus subtilis]</td><td>65</td><td>41</td><td>621</td></tr>
<tr><td>111</td><td>6</td><td>6635</td><td>6186</td><td>gnl|PID|e246063</td><td>NM23/nucleoside diphosphate kinase [Xenopus laevis]</td><td>65</td><td>50</td><td>450</td></tr>
<tr><td>116</td><td>1</td><td>3</td><td>1016</td><td>gnl|PID|d101125</td><td>queuosine biosynthesis protein QueA [Synechocystis sp.]</td><td>65</td><td>44</td><td>1014</td></tr>
<tr><td>123</td><td>1</td><td>69</td><td>389</td><td>gi|498839</td><td>ORF2 [Clostridium perfringens]</td><td>65</td><td>36</td><td>321</td></tr>
<tr><td>123</td><td>7</td><td>6522</td><td>7190</td><td>gi|1575577</td><td>DNA-binding response regulator [Thermotoga maritima]</td><td>65</td><td>39</td><td>669</td></tr>
<tr><td>125</td><td>3</td><td>3821</td><td>2859</td><td>gnl|PID|e257609</td><td>sugar-binding transport protein [Anaerocellum thermophilum]</td><td>65</td><td>47</td><td>963</td></tr>
<tr><td>137</td><td>12</td><td>8015</td><td>7818</td><td>gi|2182574</td><td>(AE000090) Y4pE [Rhizobium sp. NGR234]</td><td>65</td><td>41</td><td>198</td></tr>
<tr><td>147</td><td>4</td><td>5021</td><td>3885</td><td>gi|472329</td><td>dihydrolipoamide acetyltransferase [Clostridium magnum]</td><td>65</td><td>47</td><td>1137</td></tr>
<tr><td>148</td><td>2</td><td>1053</td><td>1931</td><td>gnl|PID|d101319</td><td>YqgH [Bacillus subtilis]</td><td>65</td><td>42</td><td>879</td></tr>
<tr><td>151</td><td>2</td><td>3212</td><td>4687</td><td>gi|304897</td><td>EcoE type I restriction modification enzyme M subunit [Escherichia coli]</td><td>65</td><td>50</td><td>1476</td></tr>
<tr><td>156</td><td>2</td><td>730</td><td>437</td><td>gi|310893</td><td>membrane protein [Theileria parva]</td><td>65</td><td>47</td><td>294</td></tr>
<tr><td>164</td><td>7</td><td>4256</td><td>4837</td><td>gi|410132</td><td>ORFX8 [Bacillus subtilis]</td><td>65</td><td>48</td><td>582</td></tr>
<tr><td>169</td><td>6</td><td>3192</td><td>3914</td><td>gi|1552737</td><td>similar to purine nucleoside phosphorylase (deoD) [Escherichia coli]</td><td>65</td><td>41</td><td>723</td></tr>
<tr><td>176</td><td>4</td><td>2951</td><td>2220</td><td>gnl|PID|e339500</td><td>oligopeptide binding lipoprotein [Streptococcus pneumoniae]</td><td>65</td><td>43</td><td>732</td></tr>
<tr><td>195</td><td>4</td><td>4556</td><td>3900</td><td>gi|1592142</td><td>ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]</td><td>65</td><td>40</td><td>657</td></tr>
<tr><td>196</td><td>1</td><td>160</td><td>1572</td><td>gnl|PID|d102004</td><td>(AB001488) PROBABLE UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2, 6-DIAMINOLIGASE (EC 6.3.2.15). [Bacillus subtilis]</td><td>65</td><td>51</td><td>1413</td></tr>
<tr><td>204</td><td>2</td><td>2246</td><td>1215</td><td>gi|143156</td><td>membrane bound protein [Bacillus subtilis]</td><td>65</td><td>37</td><td>1032</td></tr>
<tr><td>210</td><td>4</td><td>1544</td><td>1891</td><td>gi|49315</td><td>ORF1 gene product [Bacillus subtilis]</td><td>65</td><td>48</td><td>348</td></tr>
<tr><td>242</td><td>2</td><td>1625</td><td>723</td><td>gi|1787540</td><td>(AE000226) f249; This 249 aa orf is 32 pct identical (8 gaps) to 244 residues of an approx. 272 aa protein AGAR_ECOLI SW: P42902 [Escherichia coli]</td><td>65</td><td>42</td><td>903</td></tr>
</table>

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
284	1	1	900	gi|559861	clyM [Plasmid pAD1]	65	36	900
304	1	2	574	gnl|PID|e290934	unknown [Mycobacterium tuberculosis]	65	52	573
315	1	2	1483	gi|790694	mannuronan C-5-epimerase [Azotobacter vinelandii]	65	57	1482
320	1	3	569	gnl|PID|d102048	K. aerogenes, histidine utilization repressor; P12380 (199) DNA binding [Bacillus subtilis]	65	46	567
358	1	1	309	gnl|PID|e323508	YloS protein [Bacillus subtilis]	65	55	309
2	7	7571	6696	gi|1498753	nicotinate-nucleotide pyrophosphorylase [Rhodospirillum rubrum]	64	47	876
6	6	5924	6802	gnl|PID|d101111	methionine aminopeptidase [Synechocystis sp.]	64	52	879
8	4	3417	3686	gi|1045935	DNA helicase II [Mycoplasma genitalium]	64	58	270
11	4	3249	2689	gnl|PID|e265529	OrfB [Streptococcus pneumoniae]	64	46	561
15	7	6504	7145	gi|1762328	Ycr59c/YigZ homolog [Bacillus subtilis]	64	45	642
22	11	9548	9895	gnl|PID|d100581	unknown [Bacillus subtilis]	64	38	348
22	30	22503	23174	gi|289260	comE ORF1 [Bacillus subtilis]	64	44	672
26	7	14375	14199	gi|409286	bmrU [Bacillus subtilis]	64	30	177
27	2	1510	1334	gi|40795	DdeI methylase [Desulfovibrio vulgaris]	64	51	177
29	2	614	297	gi|2326168	type VII collagen [Mus musculus]	64	50	318
35	2	368	721	pir|JC1151|JC11	hypothetical 20.3K protein (insertion sequence IS1131) - Agrobacterium tumefaciens (strain PO22) plasmid Ti	64	50	354
40	1	3	449	gi|46970	epiD gene product [Staphylococcus epidermidis]	64	41	447
40	7	4683	4976	gnl|PID|e325792	(AJ000005) glucose kinase [Bacillus megaterium]	64	45	294
45	7	8068	6920	gnl|PID|d102036	subunit of ADP-glucose pyrophosphorylase [Bacillus stearothermophilus]	64	40	1149
51	2	301	1059	gi|43985	nifS-like gene [Lactobacillus delbrueckii]	64	54	759
51	13	15251	18397	gi|2293260	(AF008220) DNA-polymerase III alpha-chain [Bacillus subtilis]	64	46	3147
53	3	1157	555	gi|1574292	hypothetical [Haemophilus influenzae]	64	47	603
58	2	4236	1606	gi|1573826	alanyl-tRNA synthetase (alaS) [Haemophilus influenzae]	64	51	2631
66	1	3	1259	gi|895749	putative cellobiose phosphotransferase enzyme II'' [Bacillus subtilis]	64	42	1257
68	5	5213	6556	gi|436965	[malA] gene products [Bacillus stearothermophilus]	64	47	1344
69	6	5356	4949	gnl|PID|d101316	Cdd [Bacillus subtilis]	64	52	408

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
74	4	6948	5038	gi|726480	L-glutamine-D-fructose-6-phosphate amidotransferase [Bacillus subtilis]	64	50	1911
75	3	1283	1465	bbs|133379	TLS-CHOP=fusion protein(CHOP=C/EBP transcription factor, TLS=nuclear RNA-binding protein) [human, myxoid liposarcomas cells, Peptide Mutant, 462 aa] [Homo sapiens]	64	57	183
81	13	14016	14231	gi|143175	methanol dehydrogenase alpha-10 subunit [Bacillus sp.]	64	35	216
83	22	21851	22090	gnl|PID|d101315	YqfA [Bacillus subtilis]	64	44	240
87	11	10046	9300	gnl|PID|e323505	putative Ptc1 protein [Bacillus subtilis]	64	43	747
98	7	5032	5706	gnl|PID|e233880	hypothetical protein [Bacillus subtilis]	64	38	675
105	1	2	1276	gi|1657503	similar to S. aureus mercury(II) reductase [Escherichia coli]	64	45	1275
113	7	5136	6410	gnl|PID|d101119	NifS [Synechocystis sp.]	64	50	1275
119	1	2	1297	gnl|PID|e320520	hypothetical protein [Natronobacterium pharaonis]	64	37	1296
123	3	1125	2156	gnl|PID|e253284	ORF YDL244w [Saccharomyces cerevisiae]	64	40	1032
124	5	2331	1780	gnl|PID|d101884	hypothetical protein [Synechocystis sp.]	64	50	552
129	4	3467	2709	gnl|PID|d101314	YqeU [Bacillus subtilis]	64	52	759
131	1	152	3	gi|1377841	unknown [Bacillus subtilis]	64	42	150
137	11	7196	7549	pir|JC1151|JC11	hypothetical 20.3K protein (insertion sequence IS1131) - Agrobacterium tumefaciens (strain PO22) plasmid Ti	64	50	354
139	3	3226	2651	gi|2293301	(AF008220) YtqB [Bacillus subtilis]	64	44	576
146	10	6730	5648	gi|1322245	mevalonate pyrophosphate decarboxylase [Rattus norvegicus]	64	45	1083
147	1	2	1018	gnl|PID|e137033	unknown gene product [Lactobacillus leichmannii]	64	46	1017
148	11	8430	8783	gi|2130630	(AF000430) dynamin-like protein [Homo sapiens]	64	28	354
156	7	4313	3612	gnl|PID|d102050	transmembrane [Bacillus subtilis]	64	31	702
157	4	1299	2114	gnl|PID|d100892	homologous to Gln transport system permease proteins [Bacillus subtilis]	64	43	816
162	6	5880	6362	gi|517204	ORF1, putative 42 kDa protein [Streptococcus pyogenes]	64	58	483
164	13	9707	8769	gnl|PID|d100964	homologue of ferric anguibactin transport system permerase protein FatD of V. anguillarum [Bacillus subtilis]	64	40	939
175	5	3906	4598	gi|534045	antiterminator [Bacillus subtilis]	64	39	693
189	10	6154	6507	gi|581307	response regulator [Lactobacillus plantarum]	64	33	354
191	4	3519	2863	gi|149520	phosphoribosyl anthranilate isomerase [Lactococcus lactis]	64	46	657

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
202	1	76	1140	gnl|PID|e293806	O-acetylhomoserine sulfhydrylase [Leptospira meyeri]	64	47	1065
224	1	234	1571	gi|1573393	collagenase (prtC) [Haemophilus influenzae]	64	42	1338
231	3	291	647	gi|40174	ORF X [Bacillus subtilis]	64	43	357
253	3	709	1089	pir|JC1151|JC11	hypothetical 20.3K protein (insertion sequence IS1131) - Agrobacterium tumefaciens (strain PO22) plasmid Ti	64	50	381
265	1	820	2	gi|1377832	unknown [Bacillus subtilis]	64	31	819
297	1	1	660	gi|1590871	collagenase [Methanococcus jannaschii]	64	48	660
328	1	263	21	gi|992651	Gin4p [Saccharomyces cerevisiae]	64	41	243
5	4	8730	8098	gi|556885	Unknown [Bacillus subtilis]	63	48	633
10	6	5178	4483	gi|1573101	hypothetical [Haemophilus influenzae]	63	40	696
12	11	9324	9902	gi|806536	membrane protein [Bacillus acidopullulyticus]	63	42	579
15	10	8897	9187	gi|722339	unknown [Acetobacter xylinum]	63	40	291
17	2	1031	309	gnl|PID|e217602	PlnU [Lactobacillus plantarum]	63	32	723
18	8	7778	6975	gi|1377843	unknown [Bacillus subtilis]	63	45	804
26	4	9780	7078	gi|142440	ATP-dependent nuclease [Bacillus subtilis]	63	46	2703
29	5	3488	4192	gi|1377829	unknown [Bacillus subtilis]	63	35	705
34	11	8830	7988	gnl|PID|d101198	ORF8 [Enterococcus faecalis]	63	45	843
35	3	1187	876	gi|722339	unknown [Acetobacter xylinum]	63	39	312
48	15	12509	11691	gi|1573389	hypothetical [Haemophilus influenzae]	63	41	819
51	11	12719	12189	gi|142450	ahrC protein [Bacillus subtilis]	63	35	531
55	4	3979	5022	gi|1708640	YeaB [Bacillus subtilis]	63	41	1044
55	15	13669	14670	gnl|PID|e311502	thioredoxine reductase [Bacillus subtilis]	63	44	1002
68	10	9242	8919	sp|P37686|YIAY_	HYPOTHETICAL 40.2 KD PROTEIN IN AVTA-SELB INTERGENIC REGION (F382).	63	40	324
86	7	6554	5685	gi|1574382	lic-1 operon protein (licD) [Haemophilus influenzae]	63	41	870
88	8	6085	5180	gi|2098719	putative fimbrial-associated protein [Actinomyces naeslundii]	63	43	906
96	8	5858	6484	gi|1052803	orf1gyrb gene product [Streptococcus pneumoniae]	63	38	627
100	1	240	1940	gi|7171	fucosidase [Dictyostelium discoideum]	63	36	1701

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
104	4	3063	5765	gi|144985	phosphoenolpyruvate carboxylase [Corynebacterium glutamicum]	63	46	2703
106	8	9189	8554	gi|533099	endonuclease III [Bacillus subtilis]	63	45	636
122	6	4704	4886	gnl|PID|d101139	transposase [Synechocystis sp.]	63	39	183
128	7	4517	5203	gnl|PID|d101434	orf2 [Methanobacterium thermoautotrophicum]	63	50	687
137	4	963	1547	gi|472920	v-type Na-ATPase [Enterococcus hirae]	63	27	585
142	7	4100	4585	gnl|PID|e313025	hypothetical protein [Bacillus subtilis]	63	44	486
159	5	1741	2571	gi|1787043	(AE000184) f271; This 271 aa orf is 24 pct identical (16 gaps) to 265 residues of an approx. 272 aa protein YIDA_ECOLI SW: P09997 [Escherichia coli]	63	39	831
171	12	8803	14406	gnl|PID|e324918	IgA1 protease [Streptococcus sanguis]	63	48	5604
177	1	3	347	gi|1773150	hypothetical 14.8kd protein [Escherichia coli]	63	34	345
178	2	423	917	gi|722339	unknown [Acetobacter xylinum]	63	41	495
178	3	794	1012	gi|1591582	cobalamin biosynthesis protein N [Methanococcus jannaschii]	63	36	219
195	1	1377	175	gnl|PID|e324217	ftsQ [Enterococcus hirae]	63	33	1203
234	5	1739	1527	gi|1591582	cobalamin biosynthesis protein N [Methanococcus jannaschii]	63	36	213
249	1	81	257	gi|1000453	TreR [Bacillus subtilis]	63	41	177
283	1	127	1347	gi|396486	ORF8 [Bacillus subtilis]	63	44	1221
293	3	2804	3466	gi|722339	unknown [Acetobacter xylinum]	63	37	663
311	1	905	486	gi|1877424	UDP-galactose 4-epimerase [Streptococcus mutans]	63	46	420
324	1	2	556	gi|1477741	histidine periplasmic binding protein P29 [Campylobacter jejuni]	63	36	555
365	1	219	13	gi|2252843	(AF013293) No definition line found [Arabidopsis thaliana]	63	33	207
382	1	88	378	gi|722339	unknown [Acetobacter xylinum]	63	40	291
385	3	364	158	gi|2252843	(AF013293) No definition line found [Arabidopsis thaliana]	63	33	207
2	1	2495	288	gnl|PID|e325007	penicillin-binding protein [Bacillus subtilis]	62	42	2208
3	23	23374	24231	gnl|PID|e254993	hypothetical protein [Bacillus subtilis]	62	35	858
6	16	14320	13193	gnl|PID|e349614	nifS-like protein [Mycobacterium leprae]	62	37	1128
7	8	6819	7232	gnl|PID|d101324	YqhY [Bacillus subtilis]	62	32	414
7	19	15466	14207	gnl|PID|d101804	beta ketoacyl-acyl carrier protein synthase [Synechocystis sp.]	62	43	1260

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
7	21	17155	16229	gnl|PID|e323514	putative FabD protein [Bacillus subtilis]	62	46	927
7	24	19526	18519	gi|1276434	beta-ketoacyl-ACP synthase III [Cuphea wrightii]	62	37	1008
12	7	5904	4702	gi|1573768	A/G-specific adenine glycosylase (mutY) [Haemophilus influenzae]	62	43	1203
12	9	8032	8793	gi|1591587	pantothenate metabolism flavoprotein [Methanococcus jannaschii]	62	33	762
15	11	9678	9328	pir|JC1151|JC11	hypothetical 20.3K protein (insertion sequence IS1131) - Agrobacterium tumefaciens (strain PO22) plasmid Ti	62	43	351
17	4	2609	2442	gi|1591081	M. jannaschii predicted coding region MJ0374 [Methanococcus jannaschii]	62	43	168
17	5	3053	2835	gi|149570	role in the expression of lactacin F, part of the laf operon [Lactobacillus sp.]	62	44	219
22	10	8627	9538	gnl|PID|d100580	similar to B. subtilis DnaH [Bacillus subtilis]	62	43	912
30	3	865	2043	gi|2314379	(AE000627) ABC transporter, ATP-binding protein (yhcG) [Helicobacter pylori]	62	43	1179
33	5	2235	1636	gi|413976	ipa-52r gene product [Bacillus subtilis]	62	44	600
38	11	5689	6123	gi|148231	o251 [Escherichia coli]	62	34	435
40	17	14272	13328	gnl|PID|d101904	hypothetical protein [Synechocystis sp.]	62	43	945
42	1	3	311	gi|1146182	putative [Bacillus subtilis]	62	41	309
44	2	1267	4005	gi|1786952	(AE000176) o877; 100 pct identical to the first 86 residues of the 100 aa hypothetical protein fragment YBGB_ECOLI SW: P54746 [Escherichia coli]	62	43	2739
48	12	9732	9304	gi|662920	repressor protein [Enterococcus hirae]	62	32	429
51	8	5664	7181	gnl|PID|e301153	StySKI methylase [Salmonella enterica]	62	44	1518
52	3	2791	2099	gi|1183886	integral membrane protein [Bacillus subtilis]	62	41	693
55	16	15702	14704	gnl|PID|e313028	hypothetical protein [Bacillus subtilis]	62	40	999
59	6	3418	3984	gi|2065483	unknown [Lactococcus lactis lactis]	62	32	567
63	5	4997	4809	gi|149771	pilin gene inverting protein (PivML) [Moraxella lacunata]	62	28	189
70	14	10002	10739	gi|992977	bplG gene product [Bordetella pertussis]	62	45	738
71	13	18790	20382	gi|1280135	coded for by C. elegans cDNA cm21e6; coded for by C. elegans cDNA cm01e2; similar to melibiose carrier protein (thiomethylgalactoside permease II) [Caenorhabditis elegans]	62	62	1593
71	28	32217	32768	gnl|PID|d101312	YqeG [Bacillus subtilis]	62	35	552
74	7	11666	10383	gi|1552753	hypothetical [Escherichia coli]	62	38	1284

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
80	8	9370	9609	gnl|PID|d102002	(AB001488) FUNCTION UNKNOWN. [Bacillus subtilis]	62	46	240
97	10	9068	7041	gi|882463	protein-N(pi)-phosphohistidine-sugar phosphotransferase [Escherichia coli]	62	42	2028
98	4	2306	3268	gnl|PID|d101496	BraE (integral membrane protein) [Pseudomonas aeruginosa]	62	42	963
102	3	2823	3539	gnl|PID|e313010	hypothetical protein [Bacillus subtilis]	62	24	717
103	3	2795	1242	gnl|PID|d102049	H. influenzae hypothetical ABC transporter; P44808 (974) [Bacillus subtilis]	62	41	1554
111	2	2035	3462	gi|581297	NisP [Lactococcus lactis]	62	44	1428
112	4	3154	4080	gi|1574379	lic-1 operon protein (licA) [Haemophilus influenzae]	62	39	927
112	6	4939	5649	gi|1574381	lic-1 operon protein (licC) [Haemophilus influenzae]	62	39	711
124	3	1137	721	gi|1573024	anaerobic ribonucleoside-triphosphate reductase (nrdD) [Haemophilus influenzae]	62	45	417
124	6	3162	2329	gi|609076	leucyl aminopeptidase [Lactobacillus delbrueckii]	62	40	834
126	7	11073	7516	gnl|PID|d101163	ORF4 [Bacillus subtilis]	62	38	3558
129	6	4983	4540	pir|S41509|S415	zinc finger protein EF6 - Chilo iridescent virus	62	48	444
131	7	4510	4103	gi|1857245	unknown [Lactococcus lactis]	62	42	408
149	2	1923	2579	gi|1592142	ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]	62	41	657
149	7	5360	6055	gnl|PID|e323508	YloS protein [Bacillus subtilis]	62	40	696
156	1	450	238	gnl|PID|e254644	membrane protein [Streptococcus pneumoniae]	62	40	213
156	6	3606	2935	gnl|PID|d102050	transmembrane [Bacillus subtilis]	62	37	672
171	2	1779	2291	gi|43941	EIII-B Sor PTS [Klebsiella pneumoniae]	62	35	513
172	2	385	723	gi|895750	putative cellobiose phosphotransferase enzyme III [Bacillus subtilis]	62	39	339
173	3	2599	893	gi|1591732	cobalt transport ATP-binding protein O [Methanococcus jannaschii]	62	42	1707
179	2	492	1754	gi|1574071	H. influenzae predicted coding region HI1038 [Haemophilus influenzae]	62	38	1263
181	6	2856	3707	gi|1777435	LacT [Lactobacillus casei]	62	42	852
185	2	2074	311	gi|2182397	(AE000073) Y4fN [Rhizobium sp. NGR234]	62	41	1764
200	2	1061	1984	gi|450566	transmembrane protein [Bacillus subtilis]	62	37	924
202	3	2583	3473	gi|42219	P35 gene product (AA 1 - 314) [Escherichia coli]	62	41	891
210	3	1374	1565	gi|49315	ORF1 gene product [Bacillus subtilis]	62	45	192

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

<table>
<tr><th>Contig ID</th><th>ORF ID</th><th>Start (nt)</th><th>Stop (nt)</th><th>match acession</th><th>match gene name</th><th>% sim</th><th>% ident</th><th>length (nt)</th></tr>
<tr><td>211</td><td>1</td><td>3</td><td>971</td><td>gi|147402</td><td>mannose permease subunit III-Man [Escherichia coli]</td><td>62</td><td>43</td><td>969</td></tr>
<tr><td>223</td><td>2</td><td>1495</td><td>1034</td><td>gnl|PID|d101190</td><td>ORF2 [Streptococcus mutans]</td><td>62</td><td>41</td><td>462</td></tr>
<tr><td>228</td><td>1</td><td>34</td><td>909</td><td>gi|530063</td><td>glycerol uptake facilitator [Streptococcus pneumoniae]</td><td>62</td><td>44</td><td>876</td></tr>
<tr><td>234</td><td>2</td><td>90</td><td>917</td><td>gi|2293259</td><td>(AF008220) YtqI [Bacillus subtilis]</td><td>62</td><td>38</td><td>828</td></tr>
<tr><td>282</td><td>5</td><td>1765</td><td>1487</td><td>gnl|PID|e276475</td><td>galactokinase [Arabidopsis thaliana]</td><td>62</td><td>33</td><td>279</td></tr>
<tr><td>375</td><td>1</td><td>1</td><td>159</td><td>gi|1674231</td><td>(AE000052) Mycoplasma pneumoniae, hypothetical protein homolog; similar to Swiss-Prot Accession Number P35155, from B. subtilis [Mycoplasma pneumoniae]</td><td>62</td><td>40</td><td>159</td></tr>
<tr><td>385</td><td>5</td><td>584</td><td>357</td><td>gi|1573353</td><td>outer membrane integrity protein (tolA) [Haemophilus influenzae]</td><td>62</td><td>47</td><td>228</td></tr>
<tr><td>3</td><td>19</td><td>18550</td><td>19269</td><td>gi|606162</td><td>ORF_f229 [Escherichia coli]</td><td>61</td><td>41</td><td>720</td></tr>
<tr><td>7</td><td>4</td><td>2725</td><td>3225</td><td>gi|2114425</td><td>similar to Synechocystis sp. hypothetical protein, encoded by GenBank Accession Number D64006 [Bacillus subtilis]</td><td>61</td><td>42</td><td>501</td></tr>
<tr><td>17</td><td>6</td><td>3326</td><td>3054</td><td>gi|149569</td><td>lactacin F [Lactobacillus sp.]</td><td>61</td><td>43</td><td>273</td></tr>
<tr><td>44</td><td>3</td><td>4061</td><td>4957</td><td>gnl|PID|d101068</td><td>xylose repressor [Synechocystis sp.]</td><td>61</td><td>38</td><td>897</td></tr>
<tr><td>54</td><td>11</td><td>8388</td><td>7234</td><td>gnl|PID|d101329</td><td>YqjH [Bacillus subtilis]</td><td>61</td><td>42</td><td>1155</td></tr>
<tr><td>57</td><td>6</td><td>3974</td><td>6037</td><td>gnl|PID|d101316</td><td>YqfK [Bacillus subtilis]</td><td>61</td><td>42</td><td>2064</td></tr>
<tr><td>58</td><td>5</td><td>7356</td><td>6565</td><td>sp|P45169|POTC_</td><td>SPERMIDINE/PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTC.</td><td>61</td><td>34</td><td>792</td></tr>
<tr><td>67</td><td>1</td><td>3</td><td>692</td><td>gi|537108</td><td>ORF_f254 [Escherichia coli]</td><td>61</td><td>46</td><td>690</td></tr>
<tr><td>68</td><td>9</td><td>8816</td><td>7890</td><td>gi|19501</td><td>pPLZ12 gene product (AA 1-184) [Lupinus polyphyllus]</td><td>61</td><td>41</td><td>927</td></tr>
<tr><td>70</td><td>15</td><td>10737</td><td>12008</td><td>gi|992976</td><td>bplF gene product [Bordetella pertussis]</td><td>61</td><td>44</td><td>1272</td></tr>
<tr><td>72</td><td>11</td><td>9759</td><td>10202</td><td>gnl|PID|d101833</td><td>carboxynorspermidine decarboxylase [Synechocystis sp.]</td><td>61</td><td>36</td><td>444</td></tr>
<tr><td>76</td><td>8</td><td>7881</td><td>7003</td><td>gnl|PID|d100305</td><td>farnesyl diphosphate synthase [Bacillus stearothermophilus]</td><td>61</td><td>45</td><td>879</td></tr>
<tr><td>87</td><td>4</td><td>4914</td><td>3697</td><td>gi|528991</td><td>unknown [Bacillus subtilis]</td><td>61</td><td>42</td><td>1218</td></tr>
<tr><td>87</td><td>13</td><td>12311</td><td>11361</td><td>gi|1789683</td><td>(AE000407) methionyl-tRNA formyltransferase [Escherichia coli]</td><td>61</td><td>44</td><td>951</td></tr>
<tr><td>91</td><td>2</td><td>731</td><td>2989</td><td>gi|537080</td><td>ribonucleoside triphosphate reductase [Escherichia coli]</td><td>61</td><td>45</td><td>2259</td></tr>
<tr><td>105</td><td>3</td><td>2711</td><td>3499</td><td>gnl|PID|d101851</td><td>hypothetical protein [Synechocystis sp.]</td><td>61</td><td>44</td><td>789</td></tr>
<tr><td>115</td><td>6</td><td>7968</td><td>6478</td><td>gi|895747</td><td>putative cel operon regulator [Bacillus subtilis]</td><td>61</td><td>36</td><td>1491</td></tr>
<tr><td>123</td><td>8</td><td>7181</td><td>8518</td><td>gi|1209527</td><td>protein histidine kinase [Enterococcus faecalis]</td><td>61</td><td>40</td><td>1338</td></tr>
</table>

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
126	6	7525	6725	gi|1787043	(AE000184) f271; This 271 aa orf is 24 pct identical (16 gaps) to 265 residues of an approx. 272 aa protein YIDA_ECOLI SW: P09997 [Escherichia coli]	61	38	801
128	1	1	639	gnl|PID|d101328	YqiY [Bacillus subtilis]	61	41	639
139	7	4794	5054	gi|1022726	unknown [Staphylococcus haemolyticus]	61	41	261
139	9	12632	5913	gnl|PID|e270014	beta-galactosidase [Thermoanaerobacter ethanolicus]	61	41	6720
143	1	2552	42	gi|520541	penicillin-binding proteins 1A and 1B [Bacillus subtilis]	61	42	2511
148	16	12125	11424	gi|1552743	tetrahydrodipicolinate N-succinyltransferase [Escherichia coli]	61	42	702
162	3	4112	3456	gnl|PID|d101829	phosphoglycolate phosphatase [Synechocystis sp.]	61	30	657
172	3	727	1077	gnl|PID|d102048	B. subtilis, cellobiose phosphotransferase system, celA; P46318 (220) [Bacillus subtilis]	61	44	351
177	3	1101	1772	gnl|PID|d100574	unknown [Bacillus subtilis]	61	43	672
202	2	1278	2585	gi|1045831	hypothetical protein (GB:L18965_6) [Mycoplasma genitalium]	61	36	1308
224	3	2782	3144	gi|1591144	M. jannaschii predicted coding region MJ0440 [Methanococcus jannaschii]	61	30	363
225	4	3395	3766	gi|1552774	hypothetical [Escherichia coli]	61	40	372
249	2	212	802	gi|1000453	TreR [Bacillus subtilis]	61	42	591
254	2	843	484	gnl|PID|d100417	ORF120 [Escherichia coli]	61	36	360
257	1	3	350	gnl|PID|e255315	unknown [Mycobacterium tuberculosis]	61	42	348
293	4	3971	3657	pir|JC1151|JC11	hypothetical 20.3K protein (insertion sequence IS1131) - Agrobacterium tumefaciens (strain PO22) plasmid Ti	61	45	315
301	1	949	17	gi|2291209	(AF016424) contains similarity to acyltransferases [Caenorhabditis elegans]	61	33	933
373	1	1066	287	gi|393396	Tb-292 membrane associated protein [Trypanosoma brucei subgroup]	61	38	780
3	24	24473	24955	gi|537093	ORF_o153b [Escherichia coli]	60	27	483
6	5	4636	5739	gi|2293258	(AF008220) YtoI [Bacillus subtilis]	60	35	1104
6	12	11936	11187	gi|293017	ORF3 (put.); putative [Lactococcus lactis]	60	44	750
17	13	6708	6484	gi|149569	lactacin F [Lactobacillus sp.]	60	32	225
18	7	6977	5670	gi|1788140	(AE000278) o481; This 481 aa orf is 35 pct identical (19 gaps) to 309 residues of an approx. 856 aa protein NOL1_HUMAN SW: P46087 [Escherichia coli]	60	43	1308
20	15	15878	17167	gnl|PID|d100584	unknown [Bacillus subtilis]	60	44	1290

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
22	1	1	243	gnl|PID|d102050	transmembrane [Bacillus subtilis]	60	36	243
32	10	8296	8964	gi|2293275	(AF008220) YtaG [Bacillus subtilis]	60	37	669
38	15	8837	9697	gi|40023	B.subtilis genes rpmH, rnpA, 50kd, gidA and gidB [Bacillus subtilis]	60	35	861
43	6	8610	5944	gi|171787	protein kinase 1 [Saccharomyces cerevisiae]	60	36	2667
44	1	1	1269	gnl|PID|e235823	unknown [Schizosaccharomyces pombe]	60	44	1269
45	10	11138	10368	gi|397488	1,4-alpha-glucan branching enzyme [Bacillus subtilis]	60	43	771
48	19	15766	14378	gnl|PID|e205173	orf1 [Lactobacillus helveticus]	60	39	1389
48	21	16727	16951	gnl|PID|d102041	(AB002668) unnamed protein product [Haemophilus actinomycetemcomitans]	60	32	225
50	1	2	898	gnl|PID|e246537	ORF286 protein [Pseudomonas stutzeri]	60	31	897
62	2	638	1177	gnl|PID|d100587	unknown [Bacillus subtilis]	60	42	540
68	4	3590	5203	gi|1573583	H. influenzae predicted coding region HI0594 [Haemophilus influenzae]	60	36	1614
70	11	5781	6182	gnl|PID|d102014	(AB001488) SIMILAR TO YDFR GENE PRODUCT OF THIS ENTRY (YDFR_BACSU). [Bacillus subtilis]	60	33	402
70	12	6343	8133	gnl|PID|e324970	hypothetical protein [Bacillus subtilis]	60	38	1791
71	8	11701	14157	gi|580866	ipa-12d gene product [Bacillus subtilis]	60	33	2457
74	8	12509	11664	gnl|PID|d101832	phosphatidate cytidylyltransferase [Synechocystis sp.]	60	45	846
76	4	4116	3367	gi|2352096	orf; similar to serine/threonine protein phosphatase [Fervidobacterium islandicum]	60	39	750
80	4	7372	7665	gi|1786420	(AE000131) f86; 100 pct identical to GB: ECODINJ_6 ACCESSION: D38582 [Escherichia coli]	60	30	294
81	6	4073	4522	gi|147402	mannose permease subunit III-Man [Escherichia coli]	60	35	450
86	1	940	155	gi|143177	putative [Bacillus subtilis]	60	26	786
92	1	1	192	gi|396348	homoserine transsuccinylase [Escherichia coli]	60	45	192
93	14	10619	9384	gi|1788389	(AE000297) o464; This 464 aa orf is 33 pct identical (9 gaps) to 331 residues of an approx. 416 aa protein MTRC_NEIGO SW: P43505 [Escherichia coli]	60	27	1236
94	5	5548	8121	gnl|PID|e329895	(AJ000496) cyclic nucleotide-gated channel beta subunit [Rattus norvegicus]	60	50	2574
97	7	5396	4533	gi|1591396	transketolase' [Methanococcus jannaschii]	60	43	864
102	2	2081	2833	gnl|PID|e320929	hypothetical protein [Mycobacterium tuberculosis]	60	43	753

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

<table>
<tr><th>Contig ID</th><th>ORF ID</th><th>Start (nt)</th><th>Stop (nt)</th><th>match acession</th><th>match gene name</th><th>% sim</th><th>% ident</th><th>length (nt)</th></tr>
<tr><td>106</td><td>9</td><td>9773</td><td>9183</td><td>gnl|PID|e334782</td><td>YlbN protein [Bacillus subtilis]</td><td>60</td><td>31</td><td>591</td></tr>
<tr><td>113</td><td>8</td><td>6361</td><td>6837</td><td>gi|466875</td><td>nifU; B1496_C1_157 [Mycobacterium leprae]</td><td>60</td><td>43</td><td>477</td></tr>
<tr><td>115</td><td>2</td><td>2755</td><td>524</td><td>gnl|PID|e328143</td><td>(AJ000332) Glucosidase II [Homo sapiens]</td><td>60</td><td>32</td><td>2232</td></tr>
<tr><td>122</td><td>7</td><td>4763</td><td>5068</td><td>gnl|PID|d101876</td><td>transposase [Synechocystis sp.]</td><td>60</td><td>39</td><td>306</td></tr>
<tr><td>127</td><td>8</td><td>4510</td><td>5283</td><td>gi|1777938</td><td>Pgm [Treponema pallidum]</td><td>60</td><td>38</td><td>774</td></tr>
<tr><td>138</td><td>4</td><td>3082</td><td>2672</td><td>gnl|PID|e325196</td><td>hypothetical protein [Bacillus subtilis]</td><td>60</td><td>36</td><td>411</td></tr>
<tr><td>139</td><td>1</td><td>177</td><td>4</td><td>gnl|PID|d100680</td><td>ORF [Thermus thermophilus]</td><td>60</td><td>39</td><td>174</td></tr>
<tr><td>139</td><td>11</td><td>14520</td><td>13009</td><td>gi|537145</td><td>ORF_f437 [Escherichia coli]</td><td>60</td><td>30</td><td>1512</td></tr>
<tr><td>140</td><td>2</td><td>2592</td><td>1249</td><td>gi|1209527</td><td>protein histidine kinase [Enterococcus faecalis]</td><td>60</td><td>37</td><td>1344</td></tr>
<tr><td>141</td><td>1</td><td>210</td><td>1049</td><td>gi|463181</td><td>E5 ORF from bp 3842 to 4081; putative [Human papillomavirus type 33]</td><td>60</td><td>34</td><td>840</td></tr>
<tr><td>141</td><td>5</td><td>5368</td><td>6405</td><td>gi|145362</td><td>tyrosine-sensitive DAHP synthase (aroF) [Escherichia coli]</td><td>60</td><td>41</td><td>1038</td></tr>
<tr><td>142</td><td>6</td><td>3558</td><td>4049</td><td>gi|600711</td><td>putative [Bacillus subtilis]</td><td>60</td><td>37</td><td>492</td></tr>
<tr><td>148</td><td>10</td><td>7742</td><td>8713</td><td>gnl|PID|e313022</td><td>hypothetical protein [Bacillus subtilis]</td><td>60</td><td>27</td><td>972</td></tr>
<tr><td>153</td><td>5</td><td>3667</td><td>4278</td><td>gi|2293322</td><td>(AF008220) branch-chain amino acid transporter [Bacillus subtilis]</td><td>60</td><td>42</td><td>612</td></tr>
<tr><td>155</td><td>1</td><td>1413</td><td>748</td><td>gi|2104504</td><td>putative UDP-glucose dehydrogenase [Escherichia coli]</td><td>60</td><td>40</td><td>666</td></tr>
<tr><td>158</td><td>3</td><td>3116</td><td>2472</td><td>gnl|PID|d100872</td><td>a negative regulator of pho regulon [Pseudomonas aeruginosa]</td><td>60</td><td>37</td><td>645</td></tr>
<tr><td>159</td><td>3</td><td>778</td><td>1386</td><td>gnl|PID|e308090</td><td>product highly similar to Bacillus anthracis CapA protein [Bacillus subtilis]</td><td>60</td><td>48</td><td>609</td></tr>
<tr><td>163</td><td>7</td><td>8049</td><td>8468</td><td>gnl|PID|d101313</td><td>YqeN [Bacillus subtilis]</td><td>60</td><td>38</td><td>420</td></tr>
<tr><td>170</td><td>3</td><td>4130</td><td>2688</td><td>gi|1574179</td><td>H. influenzae predicted coding region HI1244 [Haemophilus influenzae]</td><td>60</td><td>39</td><td>1443</td></tr>
<tr><td>171</td><td>7</td><td>4717</td><td>5901</td><td>gi|606076</td><td>ORF_o384 [Escherichia coli]</td><td>60</td><td>44</td><td>1185</td></tr>
<tr><td>183</td><td>3</td><td>2440</td><td>2135</td><td>gi|1877427</td><td>repressor [Streptococcus pyogenes phage T12]</td><td>60</td><td>38</td><td>306</td></tr>
<tr><td>191</td><td>10</td><td>9444</td><td>8428</td><td>gi|415664</td><td>catabolite control protein [Bacillus megaterium]</td><td>60</td><td>42</td><td>1017</td></tr>
<tr><td>200</td><td>1</td><td>139</td><td>1083</td><td>gi|438462</td><td>transmembrane protein [Bacillus subtilis]</td><td>60</td><td>37</td><td>945</td></tr>
<tr><td>201</td><td>3</td><td>3895</td><td>1928</td><td>gi|475112</td><td>enzyme IIabc [Pediococcus pentosaceus]</td><td>60</td><td>39</td><td>1968</td></tr>
<tr><td>214</td><td>15</td><td>10930</td><td>10439</td><td>gi|1573407</td><td>hypothetical [Haemophilus influenzae]</td><td>60</td><td>39</td><td>492</td></tr>
<tr><td>218</td><td>4</td><td>2145</td><td>2363</td><td>gi|608520</td><td>myosin heavy chain kinase A [Dictyostelium discoideum]</td><td>60</td><td>31</td><td>219</td></tr>
</table>

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
226	4	2518	2351	gi|437705	hyaluronidase [Streptococcus pneumoniae]	60	53	168
242	1	725	3	gi|43938	Sor regulator [Klebsiella pneumoniae]	60	41	723
245	1	1	288	gi|304897	EcoE type I restriction modification enzyme M subunit [Escherichia coli]	60	56	288
251	1	905	45	gi|671632	unknown [Staphylococcus aureus]	60	36	861
259	1	969	82	gi|153794	rgg [Streptococcus gordonii]	60	32	888
260	2	1492	1662	pir|S31840|S318	probable transposase - Bacillus stearothermophilus	60	26	171
274	1	836	96	gi|1592173	N-ethylammeline chlorohydrolase [Methanococcus jannaschii]	60	40	741
308	1	463	2	gi|1787397	(AE000214) o157 [Escherichia coli]	60	43	462
318	1	3	308	gnl|PID|e137594	xerC recombinase [Lactobacillus leichmannii]	60	42	306
344	1	73	522	gi|509672	repressor protein [Bacteriophage Tuc2009]	60	32	450
5	1	576	4	gi|2293147	(AF008220) YtxM [Bacillus subtilis]	59	31	573
7	22	18140	17142	gnl|PID|e280724	unknown [Mycobacterium tuberculosis]	59	39	999
10	1	1413	4	gi|1353880	sialidase L [Macrobdella decora]	59	41	1410
15	6	6463	5156	gi|580841	F1 [Bacillus subtilis]	59	35	1308
22	2	479	1393	gi|142469	als operom regulatory protein [Bacillus subtilis]	59	34	915
22	5	2698	4614	gnl|PID|e280623	PCPA [Streptococcus pneumoniae]	59	44	1917
30	1	208	558	gnl|PID|e233868	hypothetical protein [Bacillus subtilis]	59	37	351
30	4	3678	2455	gnl|PID|e202290	unknown [Lactobacillus sake]	59	33	1224
35	13	12201	11071	gnl|PID|e238664	hypothetical protein [Bacillus subtilis]	59	35	1131
35	14	13288	12182	gi|1657647	Cap8H [Staphylococcus aureus]	59	39	1107
36	18	18076	17897	gi|1500535	M. jannaschii predicted coding region MJ1635 [Methanococcus jannaschii]	59	33	180
38	12	6172	7137	gi|2293239	(AF008220) YtxK [Bacillus subtilis]	59	34	966
42	3	1952	3361	gi|1684845	pinin [Canis familiaris]	59	40	1410
50	3	2678	1728	gnl|PID|d101329	YqjK [Bacillus subtilis]	59	41	951
56	5	1870	2388	gnl|PID|e137594	xerC recombinase [Lactobacillus leichmannii]	59	41	519
61	6	6812	5628	gnl|PID|e311516	aminotransferase [Bacillus subtilis]	59	40	1185
67	5	2382	3023	gi|1146190	2-keto-3-deoxy-6-phosphogluconate aldolase [Bacillus subtilis]	59	36	642

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
69	10	8567	8899	gi|1573628	antothenate kinase (coaA) [Haemophilus influenzae]	59	38	333
87	12	11383	10055	gnl|PID|e323504	putative Fmu protein [Bacillus subtilis]	59	44	1329
113	14	13927	15894	gi|1673731	(AE000010) Mycoplasma pneumoniae, fructose-permease IIBC component; similar to Swiss-Prot Accession Number P20966, from E. coli [Mycoplasma pneumoniae]	59	43	1968
115	8	8766	8521	gi|1590886	M. jannaschii predicted coding region MJ0110 [Methanococcus jannaschii]	59	38	246
119	2	1966	1526	gnl|PID|e209005	homologous to ORF2 in nrdEF operons of E.coli and S.typhimurium [Lactococcus lactis]	59	43	441
128	17	13438	13178	gnl|PID|e279632	unknown [Mycobacterium tuberculosis]	59	38	261
140	22	23903	23388	gi|482922	protein with homology to pail repressor of B.subtilis [Lactobacillus delbrueckii]	59	40	516
148	13	9697	9014	gnl|PID|d102005	(AB001488) FUNCTION UNKNOWN, SIMILAR PRODUCT IN H. INFLUENZAE AND SYNECHOCYSTIS. [Bacillus subtilis]	59	32	684
149	10	7213	8244	gi|710422	cmp-binding-factor 1 [Staphylococcus aureus]	59	40	1032
164	9	6993	6013	gnl|PID|d100965	ferric anguibactin-binding protein precusor FatB of V. anguillarum [Bacillus subtilis]	59	41	981
164	12	8836	7823	gnl|PID|d100964	homologue of ferric anguibactin transport system permerase protein FatC of V. anguillarum [Bacillus subtilis]	59	35	1014
177	2	401	1072	gi|289759	coded for by C. elegans cDNA CE2G3 (GenBank:Z14728); putative [Caenorhabditis elegans]	59	40	672
177	7	3841	4200	gi|2313445	(AE000551) H. pylori predicted coding region HP0342 [Helicobacter pylori]	59	38	360
183	4	2768	2508	gi|509672	repressor protein [Bacteriophage Tuc2009]	59	50	261
186	6	3398	2820	gi|606080	ORF_o290; Geneplot suggests frameshift linking to o267, not found [Escherichia coli]	59	38	579
190	3	3120	1711	gi|1613768	histidine protein kinase [Streptococcus pneumoniae]	59	32	1410
194	2	1621	1019	gnl|PID|d100579	unknown [Bacillus subtilis]	59	40	603
198	7	5205	4306	gnl|PID|e313073	hypothetical protein [Bacillus subtilis]	59	38	900
220	5	4362	3958	gnl|PID|d101322	YqhL [Bacillus subtilis]	59	46	405
242	3	1573	2367	gi|1787045	(AE000184) f308; This 308 aa orf is 35 pct identical (35 gaps) to 305 residues of an approx. 296 aa protein PFLC_ECOLI SW: P32675 [Escherichia coli]	59	42	795
247	2	1154	1480	gi|40073	ORF107 [Bacillus subtilis]	59	39	327

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
256	1	868	2	gnl|PID|d101924	hemolysin [Synechocystis sp.]	59	39	867
258	1	65	820	gi|2246532	ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	59	20	756
270	1	386	1126	gnl|PID|d102092	YfnB [Bacillus subtilis]	59	40	741
281	1	552	166	gi|666062	putative [Lactococcus lactis]	59	31	387
309	1	3	479	gi|405879	yeiH [Escherichia coli]	59	38	477
363	1	2	1894	gi|915208	gastric mucin [Sus scrofa]	59	31	1893
387	2	425	84	gi|160671	S antigen precursor [Plasmodium falciparum]	59	44	342
5	6	11223	10465	gnl|PID|d101812	LumQ [Synechocystis sp.]	58	29	759
29	4	2098	3513	gnl|PID|d100479	Na+ -ATPase subunit J [Enterococcus hirae]	58	39	1416
30	5	4058	3651	gi|39478	ATP binding protein of transport ATPases [Bacillus firmus]	58	34	408
33	6	2983	2210	gnl|PID|d101164	unknown [Bacillus subtilis]	58	45	774
36	8	5316	6179	gi|1518679	orf [Bacillus subtilis]	58	32	864
43	5	5926	3971	gi|1788150	(AE000278) protease II [Escherichia coli]	58	37	1956
46	5	3704	5221	gnl|PID|e267329	Unknown [Bacillus subtilis]	58	42	1518
48	14	11722	11066	gnl|PID|d101771	thiamin biosynthetic bifunctional enzyme [Synechocystis sp.]	58	34	657
52	1	1229	3	gnl|PID|d101291	reductase [Pseudomonas aeruginosa]	58	35	1227
53	2	702	412	gi|2313357	(AE000545) cytochrome c biogenesis protein (ccdA) [Helicobacter pylori]	58	25	291
58	4	6586	5498	gi|147329	transport protein [Escherichia coli]	58	41	1089
69	5	4934	3807	gnl|PID|e311492	unknown [Bacillus subtilis]	58	41	1128
71	27	31357	32277	gi|2408014	hypothetical protein [Schizosaccharomyces pombe]	58	33	921
72	4	3586	2882	gi|18694	nodulin-21 (AA 1-201; [Glycine max]	58	34	705
74	3	4937	4230	gi|2293252	(AF008220) YtmO [Bacillus subtilis]	58	33	708
79	4	4594	3422	gi|1217989	ORF3 [Streptococcus pneumoniae]	58	44	1173
82	8	10585	8171	gi|882711	exonuclease V alpha-subunit [Escherichia coli]	58	38	2415
86	17	16017	15337	gi|47642	5-dehydroquinate hydrolyase (3-dehydroquinase) [Salmonella typhi]	58	32	681
97	2	931	560	gi|153794	rgg [Streptococcus gordonii]	58	32	372

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
108	2	358	2724	gi|537020	vacB gene product [Escherichia coli]	58	37	2367
111	5	4593	5240	gi|1592142	ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]	58	36	648
120	3	4421	5110	gnl|PID|d101320	YqgX [Bacillus subtilis]	58	47	690
128	16	13131	12673	gi|662919	ORF U [Enterococcus hirae]	58	42	459
132	3	6174	4939	gi|1800301	macrolide-efflux determinant [Streptococcus pneumoniae]	58	35	1236
133	1	111	890	gnl|PID|e269488	Unknown [Bacillus subtilis]	58	36	780
160	11	8615	9865	gi|473901	ORF1 [Lactococcus lactis]	58	39	1251
161	6	6268	6849	gnl|PID|d101024	DJ-1 protein [Homo sapiens]	58	32	582
169	1	214	2	gnl|PID|d100447	translation elongation factor-3 [Chlorella virus]	58	31	213
187	1	487	2	gi|475114	regulatory protein [Pediococcus pentosaceus]	58	38	486
187	6	4384	4620	gi|167475	dessication-related protein [Craterostigma plantagineum]	58	55	237
190	2	1464	1640	gnl|PID|e246727	competence pheromone [Streptococcus gordonii]	58	38	177
192	2	2012	1344	gnl|PID|d100556	rat GCP360 [Rattus rattus]	58	44	669
206	1	1292	696	gnl|PID|e202579	product similar to WrbA [Lactobacillus sake]	58	35	597
216	2	2333	555	gnl|PID|e325036	hypothetical protein [Bacillus subtilis]	58	33	1779
217	5	5250	4321	gi|466474	cellobiose phosphotransferase enzyme II'' [Bacillus stearothermophilus]	58	38	930
217	7	5636	5106	gnl|PID|d102048	B. subtilis cellobiose phosphotransferase system celB; P46317 (998) transmembrane [Bacillus subtilis]	58	44	531
232	1	2	811	gi|1573777	cell division ATP-binding protein (ftsE) [Haemophilus influenzae]	58	39	810
264	1	2	715	gi|973330	NatA [Bacillus subtilis]	58	32	714
280	1	33	767	gi|1786187	(AE000111) hypothetical 29.6 kD protein in thrC-talB intergenic region [Escherichia coli]	58	31	735
306	1	845	3	gnl|PID|e334780	YlbL protein [Bacillus subtilis]	58	47	843
360	3	1556	1092	sp|P46351|YZGD_	HYPOTHETICAL 45.4 KD PROTEIN IN THIAMINASE I 5'REGION.	58	32	465
363	5	2160	1867	gi|160671	S antigen precursor [Plasmodium falciparum]	58	51	294
372	1	806	3	gi|393394	Tb-291 membrane associated protein [Trypanosoma brucei subgroup]	58	37	804
382	2	749	519	pir|JC1151|JC11	hypothetical 20.3K protein (insertion sequence IS1131) - Agrobacterium tumefaciens (strain PO22) plasmid Ti	58	41	231

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
3	9	8409	7471	gi|1499745	M. jannaschii predicted coding region MJ0912 [Methanococcus jannaschii]	57	38	939
10	10	7674	7507	gi|1737169	homologue to SKP1 [Arabidopsis thaliana]	57	30	168
11	1	2	412	gnl|PID|d100139	ORF [Acetobacter pasteurianus]	57	42	411
31	4	2032	1388	gi|2293213	(AF008220) YtpR [Bacillus subtilis]	57	37	645
33	11	6931	6449	gnl|PID|e324949	hypothetical protein [Bacillus subtilis]	57	36	483
45	5	5446	5060	gi|1592204	phosphoserine phosphatase [Methanococcus jannaschii]	57	44	387
49	7	6523	7632	gi|155369	PTS enzyme-II fructose [Xanthomonas campestris]	57	35	1110
52	6	4520	6850	gi|1574144	single-stranded-DNA-specific exonuclease (recJ) [Haemophilus influenzae]	57	35	2331
53	5	2079	1795	gi|1843580	replicase-associated polyprotein [oat blue dwarf virus]	57	46	285
63	6	5312	4995	gi|2182608	(AE000094) Y4rJ [Rhizobium sp. NGR234]	57	39	318
72	15	13883	13059	gnl|PID|d100892	homologous to SwissProt:YIDA_ECOLI hypothetical protein [Bacillus subtilis]	57	40	825
79	2	2561	1815	gnl|PID|d100965	homologue of NADPH-flavin oxidoreductase Frp of V. harveyi [Bacillus subtilis]	57	44	747
82	9	9596	9763	gi|1206045	short region of similarity to glycerophosphoryl diester phosphodiesterases [Caenorhabditis elegans]	57	35	168
86	16	15371	14493	gi|1787983	(AE000264) o288; 92 pct identical (1 gaps) to 222 residues of fragment YDIB_ECOLI SW: P28244 (223 aa) [Escherichia coli]	57	34	879
93	3	1695	1177	gi|1500003	mutator mutT protein [Methanococcus jannaschii]	57	33	519
96	6	3026	4519	gi|559882	threonine synthase [Arabidopsis thaliana]	57	43	1494
99	14	17211	18212	gi|773349	BirA protein [Bacillus subtilis]	57	44	1002
112	8	7448	7903	gi|1591393	M. jannaschii predicted coding region MJ0678 [Methanococcus jannaschii]	57	30	456
113	16	18627	18328	pir|A45605|A456	mature-parasite-infected erythrocyte surface antigen MESA - Plasmodium falciparum	57	22	300
123	2	343	1110	pir|F64149|F641	hypothetical protein HI0355 - Haemophilus influenzae (strain Rd KW20)	57	38	768
123	4	2108	2884	gnl|PID|d102148	(AB001684) sulfate transport system permease protein [Chlorella vulgaris]	57	39	777
127	10	6477	5587	gi|1573082	nitrogenase C (nifC) [Haemophilus influenzae]	57	35	891
128	13	9251	9790	gi|153692	pneumolysin [Streptococcus pneumoniae]	57	38	540
131	4	2139	1363	gi|42081	nagD gene product (AA 1-250) [Escherichia coli]	57	36	777

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

<table>
<tr><th>Contig ID</th><th>ORF ID</th><th>Start (nt)</th><th>Stop (nt)</th><th>match acession</th><th>match gene name</th><th>% sim</th><th>% ident</th><th>length (nt)</th></tr>
<tr><td>136</td><td>1</td><td>214</td><td>1221</td><td>bbs|148453</td><td>SpaA=endocarditis immunodominant antigen [Streptococcus sobrinus, MUCOB 263, Peptide, 1566 aa] [Streptococcus sobrinus]</td><td>57</td><td>44</td><td>1008</td></tr>
<tr><td>140</td><td>25</td><td>28701</td><td>26851</td><td>gi|505576</td><td>beta-glucoside permease [Bacillus subtilis]</td><td>57</td><td>38</td><td>1851</td></tr>
<tr><td>141</td><td>6</td><td>6395</td><td>7438</td><td>gi|995560</td><td>unknown [Schizosaccharomyces pombe]</td><td>57</td><td>41</td><td>1044</td></tr>
<tr><td>144</td><td>3</td><td>3231</td><td>2785</td><td>gnl|PID|d100139</td><td>ORF [Acetobacter pasteurianus]</td><td>57</td><td>42</td><td>447</td></tr>
<tr><td>155</td><td>4</td><td>5454</td><td>4564</td><td>gi|600431</td><td>glycosyl transerase [Erwinia amylovora]</td><td>57</td><td>34</td><td>891</td></tr>
<tr><td>159</td><td>9</td><td>4877</td><td>5854</td><td>gi|290509</td><td>o307 [Escherichia coli]</td><td>57</td><td>35</td><td>978</td></tr>
<tr><td>167</td><td>11</td><td>9710</td><td>9249</td><td>gnl|PID|d100139</td><td>ORF [Acetobacter pasteurianus]</td><td>57</td><td>42</td><td>462</td></tr>
<tr><td>171</td><td>6</td><td>4023</td><td>4436</td><td>gi|147402</td><td>mannose permease subunit III-Man [Escherichia coli]</td><td>57</td><td>29</td><td>414</td></tr>
<tr><td>178</td><td>4</td><td>2170</td><td>1076</td><td>gnl|PID|d102004</td><td>(AB001488) ATP-DEPENDENT RNA HELICASE DEAD HOMOLOG. [Bacillus subtilis]</td><td>57</td><td>39</td><td>1095</td></tr>
<tr><td>190</td><td>1</td><td>145</td><td>1455</td><td>gi|149420</td><td>export/processing protein [Lactococcus lactis]</td><td>57</td><td>30</td><td>1311</td></tr>
<tr><td>198</td><td>1</td><td>298</td><td>95</td><td>gi|522268</td><td>unidentified ORF22 [Bacteriophage bIL67]</td><td>57</td><td>36</td><td>204</td></tr>
<tr><td>203</td><td>2</td><td>3195</td><td>2110</td><td>gnl|PID|e283915</td><td>orf c01003 [Sulfolobus solfataricus]</td><td>57</td><td>41</td><td>1086</td></tr>
<tr><td>205</td><td>1</td><td>40</td><td>507</td><td>gi|1439527</td><td>EIIA-man [Lactobacillus curvatus]</td><td>57</td><td>28</td><td>468</td></tr>
<tr><td>214</td><td>7</td><td>4243</td><td>3797</td><td>gnl|PID|d102049</td><td>H. influenzae, ribosomal protein alanine acetyltransferase; P44305 (189) [Bacillus subtilis]</td><td>57</td><td>48</td><td>447</td></tr>
<tr><td>268</td><td>3</td><td>1767</td><td>1276</td><td>gi|43979</td><td>L.curvatus small cryptic plasmid gene for rep protein [Lactobacillus curvatus]</td><td>57</td><td>36</td><td>492</td></tr>
<tr><td>351</td><td>1</td><td>324</td><td>34</td><td>gnl|PID|e275871</td><td>T03F6.b [Caenorhabditis elegans]</td><td>57</td><td>31</td><td>291</td></tr>
<tr><td>386</td><td>1</td><td>226</td><td>2</td><td>gi|160671</td><td>S antigen precursor [Plasmodium falciparum]</td><td>57</td><td>45</td><td>225</td></tr>
<tr><td>5</td><td>5</td><td>10486</td><td>8777</td><td>gi|405857</td><td>yehU [Escherichia coli]</td><td>56</td><td>33</td><td>1710</td></tr>
<tr><td>8</td><td>5</td><td>3674</td><td>3910</td><td>gi|467199</td><td>pksC; L518_F1_2 [Mycobacterium leprae]</td><td>56</td><td>39</td><td>237</td></tr>
<tr><td>10</td><td>3</td><td>3442</td><td>1874</td><td>gnl|PID|d101907</td><td>sodium-coupled permease [Synechocystis sp.]</td><td>56</td><td>36</td><td>1569</td></tr>
<tr><td>21</td><td>1</td><td>1880</td><td>333</td><td>gi|2313949</td><td>(AE000593) osmoprotection protein (proWX) [Helicobacter pylori]</td><td>56</td><td>33</td><td>1548</td></tr>
<tr><td>22</td><td>29</td><td>21968</td><td>22456</td><td>gnl|PID|d102001</td><td>(AB001488) PROBABLE ACETYLTRANSFERASE. [Bacillus subtilis]</td><td>56</td><td>37</td><td>489</td></tr>
<tr><td>27</td><td>1</td><td>1361</td><td>3</td><td>gi|215132</td><td>ea59 (525) [Bacteriophage lambda]</td><td>56</td><td>30</td><td>1359</td></tr>
<tr><td>28</td><td>9</td><td>4667</td><td>4278</td><td>gi|1592090</td><td>DNA repair protein RAD2 [Methanococcus jannaschii]</td><td>56</td><td>29</td><td>390</td></tr>
<tr><td>33</td><td>1</td><td>3</td><td>386</td><td>gnl|PID|d100139</td><td>ORF [Acetobacter pasteurianus]</td><td>56</td><td>41</td><td>384</td></tr>
</table>

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
36	7	5122	5397	pir|PQ0053|PQ00	hypothetical protein (proC 3' region) - Pseudomonas aeruginosa (strain PAO) (fragment)	56	28	276
40	4	3137	4318	gi|1800301	macrolide-efflux determinant [Streptococcus pneumoniae]	56	27	1182
40	16	12511	13191	gnl|PID|e217602	PlnU [Lactobacillus plantarum]	56	38	681
48	17	13775	13023	gi|143729	transcription activator [Bacillus subtilis]	56	35	753
75	4	1674	2594	gnl|PID|d102036	membrane protein [Bacillus stearothermophilus]	56	25	921
85	3	1842	1459	gnl|PID|d100139	ORF [Acetobacter pasteurianus]	56	41	384
89	7	5815	4940	gi|853777	product similar to E.coli PRFA2 protein [Bacillus subtilis]	56	42	876
105	2	1360	2718	gnl|PID|d101913	hypothetical protein [Synechocystis sp.]	56	37	1359
112	3	2151	3194	gi|537201	ORF_o345 [Escherichia coli]	56	31	1044
113	4	2754	2963	gnl|PID|d100340	ORF [Plum pox virus]	56	28	210
122	3	1203	2054	gi|1649035	high-affinity periplasmic glutamine binding protein [Salmonella typhimurium]	56	30	852
124	8	3939	3694	gnl|PID|e248893	unknown [Mycobacterium tuberculosis]	56	27	246
125	4	4403	4107	gnl|PID|d100247	human non-muscle myosin heavy chain [Homo sapiens]	56	32	297
127	11	6608	6405	gi|2182397	(AE000073) Y4fN [Rhizobium sp. NGR234]	56	35	204
134	5	4769	3849	gnl|PID|d101870	hypothetical protein [Synechocystis sp.]	56	39	921
137	10	6814	7245	gi|1592011	sulfate permease (cysA) [Methanococcus jannaschii]	56	34	432
142	8	5019	4582	pir|A47071|A470	orf1 immediately 5' of nifS - Bacillus subtilis	56	29	438
146	8	4676	3660	gnl|PID|d101911	hypothetical protein [Synechocystis sp.]	56	32	1017
148	3	1906	2739	gnl|PID|d101099	phosphate transport system permease protein PstA [Synechocystis sp.]	56	36	834
150	4	4449	2743	gnl|PID|e304628	probably site-specific recombinase of the resolvase family of enzymes [Bacteriophage TP21]	56	27	1707
172	1	2	208	gi|1787791	(AE000249) f317; This 317 aa orf is 27 pct identical (16 gaps) to 301 residues of an approx. 320 aa protein YXXC_BACSU SW: P39140 [Escherichia coli]	56	34	207
172	7	4979	5668	gi|396293	similar to Bacillus subtilis hypoth. 20 kDa protein, in tsr 3' region [Escherichia coli]	56	40	690
186	7	3732	3367	gi|1732200	PTS permease for mannose subunit IIPMan [Vibrio furnissii]	56	36	366
187	2	2402	819	pir|S57904|S579	virR49 protein - Streptococcus pyogenes (strain CS101, serotype M49)	56	35	1584

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
204	3	2772	2239	gi|606376	ORF_o162 [Escherichia coli]	56	35	534
206	2	3342	1633	gi|559861	clyM [Plasmid pAD1]	56	38	1710
219	3	1689	1096	gi|1146197	putative [Bacillus subtilis]	56	27	594
230	2	409	1485	pir|C60328|C603	hypothetical protein 2 (sr 5' region) - Streptococcus mutans (strain OMZ175, serotype f)	56	40	1077
233	4	2930	3268	gi|1041785	rhoptry protein [Plasmodium yoelii]	56	24	339
273	2	1543	2724	gi|143089	iep protein [Bacillus subtilis]	56	32	1182
353	1	1	516	gnl|PID|e325000	hypothetical protein [Bacillus subtilis]	56	41	516
359	1	87	641	gi|1786952	(AE000176) o877; 100 pct identical to the first 86 residues of the 100 aa hypothetical protein fragment YBGB_ECOLI SW: P54746 [Escherichia coli]	56	46	555
363	7	4482	4198	gi|1573353	outer membrane integrity protein (tolA) [Haemophilus influenzae]	56	38	285
376	1	2	508	gnl|PID|e325031	hypothetical protein [Bacillus subtilis]	56	33	507
18	1	836	177	gnl|PID|d100872	a negative regulator of pho regulon [Pseudomonas aeruginosa]	55	31	660
28	4	1824	1618	gnl|PID|e316518	STAT protein [Dictyostelium discoideum]	55	40	207
29	6	4496	5041	gi|1088261	unknown protein [Anabaena sp.]	55	31	546
38	16	9695	10702	gi|580905	B.subtilis genes rpmH, rnpA, 50kd, gidA and gidB [Bacillus subtilis]	55	31	1008
49	5	5727	6182	gi|1786951	(AE000176) heat-responsive regulatory protein [Escherichia coli]	55	29	456
51	4	2381	3241	gnl|PID|d101293	YbbA [Bacillus subtilis]	55	42	861
52	9	9640	10866	gi|153016	ORF 419 protein [Staphylococcus aureus]	55	23	1227
53	4	1813	1349	gi|896042	OspF [Borrelia burgdorferi]	55	30	465
60	5	4794	5756	gi|1499876	magnesium and cobalt transport protein [Methanococcus jannaschii]	55	38	963
71	9	14176	15408	gi|1857120	glycosyl transferase [Neisseria meningitidis]	55	41	1233
75	6	3189	4229	gnl|PID|e209890	NAD alcohol dehydrogenase [Bacillus subtilis]	55	44	1041
108	10	10488	9820	gnl|PID|e324997	hypothetical protein [Bacillus subtilis]	55	36	669
113	12	12273	13037	gnl|PID|e311496	unknown [Bacillus subtilis]	55	34	765
113	13	13007	13945	gi|1573423	1-phosphofructokinase (fruK) [Haemophilus influenzae]	55	39	939
126	5	6764	5907	gi|1790131	(AE000446) hypothetical 29.7 kD protein in ibpA-gyrB intergenic region [Escherichia coli]	55	37	858

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
129	3	2719	902	gnl|PID|d101425	Pz-peptidase [Bacillus licheniformis]	55	35	1818
138	3	2593	1610	gi|142833	ORF2 [Bacillus subtilis]	55	37	984
140	6	6916	5633	gnl|PID|d100964	homologue of hypothetical protein in a rapamycin synthesis gene cluster of Streptomyces hygroscopicus [Bacillus subtilis]	55	26	1284
147	3	3854	2136	gi|472330	dihydrolipoamide dehydrogenase [Clostridium magnum]	55	39	1719
147	10	10204	8921	gnl|PID|e73078	dihydroorotase [Lactobacillus leichmannii]	55	38	1284
148	5	3430	4119	gi|290572	peripheral membrane protein U [Escherichia coli]	55	29	690
148	6	4171	4650	gi|695769	transposase [Xanthobacter autotrophicus]	55	37	480
149	14	12564	11650	gnl|PID|d101329	YqjG [Bacillus subtilis]	55	32	915
156	3	1113	550	gi|2314496	(AE000634) conserved hypothetical integral membrane protein [Helicobacter pylori]	55	34	564
159	10	6625	5897	gi|290533	similar to E. coli ORF adjacent to suc operon; similar to gntR class of regulatory proteins [Escherichia coli]	55	29	729
164	3	1784	2332	gnl|PID|e255118	hypothetical protein [Bacillus subtilis]	55	37	549
164	5	2772	3521	gi|40348	put. resolvase Tnp I (AA 1 - 284) [Bacillus thuringiensis]	55	35	750
164	11	7428	7216	gnl|PID|e249407	unknown [Mycobacterium tuberculosis]	55	38	213
167	5	3860	3345	gi|535052	involved in protein secretion [Bacillus subtilis]	55	28	516
186	5	2880	2563	gi|606080	ORF_o290; Geneplot suggests frameshift linking to o267, not found [Escherichia coli]	55	35	318
189	8	4311	5396	gnl|PID|e183450	hypothetical EcsB protein [Bacillus subtilis]	55	32	1086
192	5	3270	3079	gi|1196504	vitellogenin convertase [Aedes aegypti]	55	38	192
195	2	2454	1384	gi|1574693	transferase, peptidoglycan synthesis (murG) [Haemophilus influenzae]	55	33	1071
198	4	3013	2471	gnl|PID|e313074	hypothetical protein [Bacillus subtilis]	55	29	543
214	1	373	744	gnl|PID|d101741	transposase [Synechocystis sp.]	55	33	372
219	2	1115	456	gi|288301	ORF2 gene product [Bacillus megaterium]	55	30	660
263	7	3742	3443	gi|18137	cgcr-4 product [Chlamydomonas reinhardtii]	55	48	300
285	1	2	829	gnl|PID|d100974	unknown [Bacillus subtilis]	55	40	828
286	1	650	249	gi|396844	ORF (18 kDa) [Vibrio cholerae]	55	31	402
297	2	1229	1696	gi|150848	prtC [Porphyromonas gingivalis]	55	39	468

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
309	2	218	982	gi|1574491	hypothetical [Haemophilus influenzae]	55	35	765
328	2	646	224	gi|571500	prohibitin [Saccharomyces cerevisiae]	55	27	423
330	1	1340	474	gi|396397	soxS [Escherichia coli]	55	29	867
364	3	2538	1546	gi|393394	Tb-291 membrane associated protein [Trypanosoma brucei subgroup]	55	36	993
368	3	941	105	gi|160671	S antigen precursor [Plasmodium falciparum]	55	40	837
3	5	4604	3624	gi|2293176	(AF008220) signal transduction protein kinase [Bacillus subtilis]	54	26	981
9	11	7746	7246	gi|1146245	putative [Bacillus subtilis]	54	38	501
38	24	16213	17937	gi|1480429	putative transcriptional regulator [Bacillus stearothermophilus]	54	27	1725
40	8	5076	4882	gi|39989	methionyl-tRNA synthetase [Bacillus stearothermophilus]	54	35	195
43	4	3980	2367	gnl|PID|e148611	ABC transporter [Lactobacillus helveticus]	54	25	1614
52	10	10844	12103	gi|1762962	FemA [Staphylococcus simulans]	54	29	1260
57	1	3	512	gi|558177	endo-1,4-beta-xylanase [Cellulomonas fimi]	54	36	510
58	3	4749	4246	gnl|PID|d101237	hypothetical [Bacillus subtilis]	54	29	504
71	7	10684	11703	gi|510255	orf3 [Escherichia coli]	54	31	1020
71	20	27546	27737	gi|202543	serotonin receptor [Rattus norvegicus]	54	31	192
72	2	844	1098	gi|148613	srnB gene product [Plasmid F]	54	37	255
72	7	7438	6695	gi|1196496	recombinase [Moraxella bovis]	54	38	744
74	10	14043	13465	gi|1200342	ORF 3 gene product [Bradyrhizobium japonicum]	54	32	579
74	12	16483	15995	gi|2317798	maturase-related protein [Pseudomonas alcaligenes]	54	30	489
86	3	2877	2155	gi|46988	orf9.6 possibly encodes the O unit polymerase [Salmonella enterica]	54	34	723
89	5	4433	3921	gi|147211	phnO protein [Escherichia coli]	54	41	513
90	1	3	464	gi|2317798	maturase-related protein [Pseudomonas alcaligenes]	54	30	462
96	10	8058	8510	gnl|PID|d102015	(AB001488) SIMILAR TO SALMONELLA TYPHIMURIUM SLYY GENE REQUIRED FOR SURVIVAL IN MACROPHAGE. [Bacillus subtilis]	54	32	453
97	6	4662	3604	gi|1591394	transketolase'' [Methanococcus jannaschii]	54	30	1059
106	11	10406	12010	gi|606286	ORF_o637 [Escherichia coli]	54	32	1605
147	8	8663	7404	gnl|PID|d101615	ORF_ID:o319#7; similar to [SwissProt Accession Number P37340] [Escherichia coli]	54	35	1260

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
171	4	2477	3223	gi|1439528	EIIC-man [Lactobacillus curvatus]	54	36	747
174	2	2068	1787	gnl|PID|d100518	motor protein [Homo sapiens]	54	35	282
188	1	526	1188	gnl|PID|e250352	unknown [Mycobacterium tuberculosis]	54	31	663
198	5	3582	2884	gnl|PID|e313074	hypothetical protein [Bacillus subtilis]	54	33	699
207	1	1	1641	gnl|PID|d101813	hypothetical protein [Synechocystis sp.]	54	24	1641
210	1	2	655	gi|2293206	(AF008220) YtmP [Bacillus subtilis]	54	29	654
225	2	966	2357	gnl|PID|e330194	R11H6.1 [Caenorhabditis elegans]	54	39	1392
241	1	1681	347	gnl|PID|d101813	hypothetical protein [Synechocystis sp.]	54	26	1335
263	2	907	1395	gnl|PID|d101886	transposase [Synechocystis sp.]	54	30	489
263	6	3450	2977	gi|160671	S antigen precursor [Plasmodium falciparum]	54	47	474
277	3	2517	1363	gi|1196926	unknown protein [Streptococcus mutans]	54	30	1155
307	1	828	4	gi|2293198	(AF008220) YtgP [Bacillus subtilis]	54	28	825
325	1	19	768	gi|2182507	(AE000083) Y4lH [Rhizobium sp. NGR234]	54	37	750
332	2	898	590	gi|1591815	ADP-ribosylglycohydrolase (draG) [Methanococcus jannaschii]	54	32	309
385	4	240	479	gi|530878	amino acid feature: N-glycosylation sites, aa 41 .. 43, 46 .. 48, 51 .. 53, 72 .. 74, 107 .. 109, 128 .. 130, 132 .. 134, 158 .. 160, 163 .. 165; amino acid feature: Rod protein domain, aa 169 .. 340; amino acid feature: globular protein domai	54	49	240
7	25	19702	19493	gnl|PID|e255111	hypothetical protein [Bacillus subtilis]	53	32	210
23	3	2497	2033	gnl|PID|d102015	(AB001488) SIMILAR TO SALMONELLA TYPHIMURIUM SLYY GENE REQUIRED FOR SURVIVAL IN MACROPHAGE. [Bacillus subtilis]	53	25	465
29	11	9042	10121	gi|143331	alkaline phosphatase regulatory protein [Bacillus subtilis]	53	31	1080
33	3	1479	1009	pir|S10655|S106	hypothetical protein X - Pyrococcus woesei (fragment)	53	33	471
36	6	4583	5134	gnl|PID|e316029	unknown [Mycobacterium tuberculosis]	53	30	552
38	14	8521	8898	gi|580904	homologous to E.coli rnpA [Bacillus subtilis]	53	30	378
52	7	7007	8686	gi|1377831	unknown [Bacillus subtilis]	53	29	1680
54	17	17555	19564	gi|666069	orf2 gene product [Lactobacillus leichmannii]	53	36	2010
56	1	1	681	gi|1592266	restriction modification system S subunit [Methanococcus jannaschii]	53	32	681

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

<table>
<tr><th>Contig ID</th><th>ORF ID</th><th>Start (nt)</th><th>Stop (nt)</th><th>match acession</th><th>match gene name</th><th>% sim</th><th>% ident</th><th>length (nt)</th></tr>
<tr><td>57</td><td>10</td><td>9431</td><td>8487</td><td>gi|1788543</td><td>(AE000310) f351; Residues 1-121 are 100 pct identical to YOJL_ECOLI SW: P33944 (122 aa) and aa 152-351 are 100 pct identical to YOJK_ECOLI SW: P33943 [Escherichia coli]</td><td>53</td><td>31</td><td>945</td></tr>
<tr><td>61</td><td>1</td><td>429</td><td>4</td><td>gnl|PID|e236467</td><td>B0024.12 [Caenorhabditis elegans]</td><td>53</td><td>33</td><td>426</td></tr>
<tr><td>71</td><td>1</td><td>5772</td><td>4</td><td>gi|393394</td><td>Tb-291 membrane associated protein [Trypanosoma brucei subgroup]</td><td>53</td><td>33</td><td>5769</td></tr>
<tr><td>72</td><td>3</td><td>894</td><td>2840</td><td>gi|2293178</td><td>(AF008220) YtsD [Bacillus subtilis]</td><td>53</td><td>27</td><td>1947</td></tr>
<tr><td>73</td><td>14</td><td>9793</td><td>9212</td><td>gi|1778556</td><td>putative cobalamin synthesis protein [Escherichia coli]</td><td>53</td><td>32</td><td>582</td></tr>
<tr><td>88</td><td>7</td><td>5217</td><td>4342</td><td>gi|2098719</td><td>putative fimbrial-associated protein [Actinomyces naeslundii]</td><td>53</td><td>38</td><td>876</td></tr>
<tr><td>93</td><td>5</td><td>2395</td><td>1688</td><td>gi|563366</td><td>gluconate oxidoreductase [Gluconobacter oxydans]</td><td>53</td><td>33</td><td>708</td></tr>
<tr><td>96</td><td>9</td><td>6632</td><td>7762</td><td>gi|517204</td><td>ORF1, putative 42 kDa protein [Streptococcus pyogenes]</td><td>53</td><td>42</td><td>1131</td></tr>
<tr><td>108</td><td>8</td><td>7629</td><td>8600</td><td>gi|149581</td><td>maturation protein [Lactobacillus paracasei]</td><td>53</td><td>32</td><td>972</td></tr>
<tr><td>128</td><td>9</td><td>6412</td><td>6972</td><td>gnl|PID|e317237</td><td>unknown [Mycobacterium tuberculosis]</td><td>53</td><td>36</td><td>561</td></tr>
<tr><td>128</td><td>12</td><td>8429</td><td>9253</td><td>gi|311070</td><td>pentraxin fusion protein [Xenopus laevis]</td><td>53</td><td>31</td><td>825</td></tr>
<tr><td>148</td><td>1</td><td>3</td><td>950</td><td>pir|A61607|A616</td><td>probable hemolysin precursor - Streptococcus agalactiae (strain 74-360)</td><td>53</td><td>36</td><td>948</td></tr>
<tr><td>163</td><td>2</td><td>2162</td><td>3022</td><td>gi|1755150</td><td>nocturnin [Xenopus laevis]</td><td>53</td><td>30</td><td>861</td></tr>
<tr><td>171</td><td>3</td><td>2304</td><td>2624</td><td>gi|1732200</td><td>PTS permease for mannose subunit IIPMan [Vibrio furnissii]</td><td>53</td><td>32</td><td>321</td></tr>
<tr><td>182</td><td>5</td><td>3785</td><td>3051</td><td>gnl|PID|d100572</td><td>unknown [Bacillus subtilis]</td><td>53</td><td>35</td><td>735</td></tr>
<tr><td>209</td><td>3</td><td>2948</td><td>1935</td><td>gi|1778505</td><td>ferric enterobactin transport protein [Escherichia coli]</td><td>53</td><td>28</td><td>1014</td></tr>
<tr><td>218</td><td>5</td><td>3884</td><td>2406</td><td>gi|40162</td><td>murE gene product [Bacillus subtilis]</td><td>53</td><td>34</td><td>1479</td></tr>
<tr><td>250</td><td>3</td><td>473</td><td>790</td><td>gnl|PID|e334776</td><td>YlbH protein [Bacillus subtilis]</td><td>53</td><td>30</td><td>318</td></tr>
<tr><td>275</td><td>1</td><td>1</td><td>1611</td><td>gnl|PID|d101314</td><td>YqeW [Bacillus subtilis]</td><td>53</td><td>35</td><td>1611</td></tr>
<tr><td>332</td><td>1</td><td>544</td><td>2</td><td>gi|409286</td><td>bmrU [Bacillus subtilis]</td><td>53</td><td>31</td><td>543</td></tr>
<tr><td>2</td><td>2</td><td>2543</td><td>3445</td><td>gnl|PID|e233879</td><td>hypothetical protein [Bacillus subtilis]</td><td>52</td><td>39</td><td>903</td></tr>
<tr><td>3</td><td>22</td><td>22402</td><td>23376</td><td>gi|38969</td><td>lacF gene product [Agrobacterium radiobacter]</td><td>52</td><td>36</td><td>975</td></tr>
<tr><td>5</td><td>3</td><td>8094</td><td>2356</td><td>gnl|PID|e324915</td><td>IgA1 protease [Streptococcus sanguis]</td><td>52</td><td>32</td><td>5739</td></tr>
<tr><td>22</td><td>26</td><td>19961</td><td>20212</td><td>gi|152901</td><td>ORF 3 [Spirochaeta aurantia]</td><td>52</td><td>35</td><td>252</td></tr>
<tr><td>22</td><td>31</td><td>23140</td><td>24666</td><td>gi|289262</td><td>comE ORF3 [Bacillus subtilis]</td><td>52</td><td>32</td><td>1527</td></tr>
<tr><td>27</td><td>6</td><td>5397</td><td>4801</td><td>gi|39573</td><td>P20 (AA 1-178) [Bacillus licheniformis]</td><td>52</td><td>35</td><td>597</td></tr>
</table>

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

<table>
<tr><th>Contig ID</th><th>ORF ID</th><th>Start (nt)</th><th>Stop (nt)</th><th>match acession</th><th>match gene name</th><th>% sim</th><th>% ident</th><th>length (nt)</th></tr>
<tr><td>35</td><td>10</td><td>8604</td><td>7357</td><td>gi|508241</td><td>putative O-antigen transporter [Escherichia coli]</td><td>52</td><td>27</td><td>1248</td></tr>
<tr><td>45</td><td>4</td><td>4801</td><td>3662</td><td>gnl|PID|d102243</td><td>(AB005554) homologs are found in E. coli and H. influenzae; see SWISS_PROT ACC#: P42100 [Bacillus subtilis]</td><td>52</td><td>36</td><td>1140</td></tr>
<tr><td>48</td><td>18</td><td>14385</td><td>13726</td><td>gnl|PID|e205174</td><td>orf2 [Lactobacillus helveticus]</td><td>52</td><td>25</td><td>660</td></tr>
<tr><td>49</td><td>4</td><td>5321</td><td>5755</td><td>gi|2317740</td><td>(AF013987) nitrogen regulatory IIA protein [Vibrio cholerae]</td><td>52</td><td>19</td><td>435</td></tr>
<tr><td>54</td><td>4</td><td>2773</td><td>4668</td><td>gi|1500472</td><td>M. jannaschii predicted coding region MJ1577 [Methanococcus jannaschii]</td><td>52</td><td>36</td><td>1896</td></tr>
<tr><td>54</td><td>6</td><td>5250</td><td>4969</td><td>gi|2182453</td><td>(AE000079) Y4iO [Rhizobium sp. NGR234]</td><td>52</td><td>40</td><td>282</td></tr>
<tr><td>66</td><td>6</td><td>8400</td><td>6955</td><td>gi|43140</td><td>TrkG protein [Escherichia coli]</td><td>52</td><td>30</td><td>1446</td></tr>
<tr><td>71</td><td>26</td><td>30659</td><td>31312</td><td>gnl|PID|e314993</td><td>unknown [Mycobacterium tuberculosis]</td><td>52</td><td>23</td><td>654</td></tr>
<tr><td>75</td><td>2</td><td>1673</td><td>1035</td><td>gnl|PID|d102271</td><td>(AB001683) FarA [Streptomyces sp.]</td><td>52</td><td>27</td><td>639</td></tr>
<tr><td>81</td><td>3</td><td>1439</td><td>2893</td><td>gnl|PID|e311458</td><td>rhamnulose kinase [Bacillus subtilis]</td><td>52</td><td>32</td><td>1455</td></tr>
<tr><td>81</td><td>8</td><td>4987</td><td>5781</td><td>gi|147403</td><td>mannose permease subunit II-P-Man [Escherichia coli]</td><td>52</td><td>37</td><td>795</td></tr>
<tr><td>83</td><td>21</td><td>20687</td><td>21853</td><td>gi|143365</td><td>phosphoribosyl aminoimidazole carboxylase II (PUR-K; ttg start codon) [Bacillus subtilis]</td><td>52</td><td>37</td><td>1167</td></tr>
<tr><td>86</td><td>6</td><td>5785</td><td>4592</td><td>gi|1276879</td><td>EpsF [Streptococcus thermophilus]</td><td>52</td><td>26</td><td>1194</td></tr>
<tr><td>86</td><td>20</td><td>19390</td><td>17861</td><td>gi|454844</td><td>ORF 3 [Schistosoma mansoni]</td><td>52</td><td>26</td><td>1530</td></tr>
<tr><td>96</td><td>13</td><td>10540</td><td>9659</td><td>gi|288299</td><td>ORF1 gene product [Bacillus megaterium]</td><td>52</td><td>33</td><td>882</td></tr>
<tr><td>111</td><td>1</td><td>2</td><td>2026</td><td>gi|148309</td><td>cytolysin B transport protein [Enterococcus faecalis]</td><td>52</td><td>27</td><td>2025</td></tr>
<tr><td>112</td><td>2</td><td>1457</td><td>2167</td><td>gi|471234</td><td>orf1 [Haemophilus influenzae]</td><td>52</td><td>33</td><td>711</td></tr>
<tr><td>118</td><td>3</td><td>2931</td><td>2365</td><td>bbs|151233</td><td>Mip=24 kda macrophage infectivity potentiator protein [Legionella pneumophila, Philadelphia-1, Peptide, 184 aa] [Legionella pneumophila]</td><td>52</td><td>33</td><td>567</td></tr>
<tr><td>122</td><td>9</td><td>5646</td><td>5951</td><td>gi|8214</td><td>myosin heavy chain [Drosophila melanogaster]</td><td>52</td><td>36</td><td>306</td></tr>
<tr><td>122</td><td>11</td><td>6159</td><td>6374</td><td>gi|434025</td><td>dihydrolipoamide acetyltransferase [Pelobacter carbinolicus]</td><td>52</td><td>52</td><td>216</td></tr>
<tr><td>134</td><td>6</td><td>4880</td><td>6313</td><td>gi|153733</td><td>M protein trans-acting positive regulator [Streptococcus pyogenes]</td><td>52</td><td>43</td><td>1434</td></tr>
<tr><td>135</td><td>3</td><td>1238</td><td>2716</td><td>gnl|PID|e245024</td><td>unknown [Mycobacterium tuberculosis]</td><td>52</td><td>35</td><td>1479</td></tr>
<tr><td>141</td><td>3</td><td>1681</td><td>2319</td><td>gnl|PID|d100573</td><td>unknown [Bacillus subtilis]</td><td>52</td><td>32</td><td>639</td></tr>
<tr><td>161</td><td>4</td><td>2562</td><td>5024</td><td>gi|1146243</td><td>22.4% identity with Escherichia coli DNA-damage inducible protein ...; putative [Bacillus subtilis]</td><td>52</td><td>36</td><td>2463</td></tr>
<tr><td>173</td><td>2</td><td>968</td><td>183</td><td>gi|1215693</td><td>putative orf; GT9_orf434 [Mycoplasma pneumoniae]</td><td>52</td><td>30</td><td>786</td></tr>
</table>

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
198	6	4400	3567	gnl|PID|e313010	hypothetical protein [Bacillus subtilis]	52	26	834
210	12	8844	9107	gi|497647	DNA gyrase subunit B [Mycoplasma genitalium]	52	38	264
214	10	5264	5431	gi|550697	envelope protein [Human immunodeficiency virus type 1]	52	36	168
225	1	15	884	gi|1552773	hypothetical [Escherichia coli]	52	34	870
230	1	39	362	gnl|PID|d100582	unknown [Bacillus subtilis]	52	28	324
287	1	871	2	gnl|PID|e335028	protease/peptidase [Mycobacterium leprae]	52	29	870
363	2	1305	4	gi|393394	Tb-291 membrane associated protein [Trypanosoma brucei subgroup]	52	32	1302
23	2	2048	1173	gnl|PID|e254943	unknown [Mycobacterium tuberculosis]	51	30	876
29	3	742	1521	gi|929900	5'-methylthioadenosine phosphorylase [Sulfolobus solfataricus]	51	31	780
45	1	410	1597	gi|1877429	integrase [Streptococcus pyogenes phage T12]	51	32	1188
48	26	19227	18946	gi|2314455	(AE000633) transcriptional regulator (tenA) [Helicobacter pylori]	51	33	282
73	5	4276	4016	gi|474177	alpha-D-1,4-glucosidase [Staphylococcus xylosus]	51	31	261
81	11	8935	12057	gi|311070	pentraxin fusion protein [Xenopus laevis]	51	31	3123
83	5	1195	1986	gnl|PID|d101316	YqfI [Bacillus subtilis]	51	33	792
98	10	7531	8538	gi|41500	ORF 3 (AA 1-352); 38 kD (put. ftsX) [Escherichia coli]	51	28	1008
113	6	3908	5173	gi|466882	pps1; B1496_C2_189 [Mycobacterium leprae]	51	27	1266
124	1	326	57	gi|2191168	(AF007270) contains similarity to myosin heavy chain [Arabidopsis thaliana]	51	32	270
129	10	7286	6816	gi|1046241	orf14 [Bacteriophage HP1]	51	30	471
143	3	4963	3983	gi|1354935	probable copper-transporting atpase [Escherichia coli]	51	26	981
148	15	11359	10226	gi|2293256	(AF008220) putative hippurate hydrolase [Bacillus subtilis]	51	36	1134
149	8	6003	7313	gi|1633572	Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]	51	21	1311
151	9	12092	11550	gnl|PID|e281580	hypothetical 40.7 kd protein [Bacillus subtilis]	51	34	543
159	6	2555	3208	gi|146944	CMP-N-acetylneuraminic acid synthetase [Escherichia coli]	51	36	654
174	1	1797	4	gi|1773166	probable copper-transporting atpase [Escherichia coli]	51	28	1794
265	4	2231	1773	gnl|PID|e256400	anti-P.falciparum antigenic polypeptide [Saimiri sciureus]	51	18	459
277	2	643	1311	pir|S32915|S329	pilD protein - Neisseria gonorrhoeae	51	33	669

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

<table>
<tr><th>Contig ID</th><th>ORF ID</th><th>Start (nt)</th><th>Stop (nt)</th><th>match acession</th><th>match gene name</th><th>% sim</th><th>% ident</th><th>length (nt)</th></tr>
<tr><td>350</td><td>1</td><td>890</td><td>3</td><td>gi|290509</td><td>o307 [Escherichia coli]</td><td>51</td><td>30</td><td>888</td></tr>
<tr><td>363</td><td>4</td><td>1228</td><td>4485</td><td>gi|1707247</td><td>partial CDS [Caenorhabditis elegans]</td><td>51</td><td>23</td><td>3258</td></tr>
<tr><td>367</td><td>1</td><td>1701</td><td>4</td><td>gi|393394</td><td>Tb-291 membrane associated protein [Trypanosoma brucei subgroup]</td><td>51</td><td>32</td><td>1698</td></tr>
<tr><td>15</td><td>5</td><td>5174</td><td>4497</td><td>gnl|PID|e58151</td><td>F3 [Bacillus subtilis]</td><td>50</td><td>38</td><td>678</td></tr>
<tr><td>16</td><td>4</td><td>2220</td><td>2582</td><td>gnl|PID|e325010</td><td>hypothetical protein [Bacillus subtilis]</td><td>50</td><td>29</td><td>363</td></tr>
<tr><td>19</td><td>5</td><td>2591</td><td>4159</td><td>gi|1552733</td><td>similar to voltage-gated chloride channel protein [Escherichia coli]</td><td>50</td><td>30</td><td>1569</td></tr>
<tr><td>25</td><td>4</td><td>2701</td><td>1997</td><td>gi|887849</td><td>ORF_f219 [Escherichia coli]</td><td>50</td><td>27</td><td>705</td></tr>
<tr><td>35</td><td>1</td><td>211</td><td>417</td><td>gnl|PID|e236697</td><td>unknown [Saccharomyces cerevisiae]</td><td>50</td><td>33</td><td>207</td></tr>
<tr><td>39</td><td>4</td><td>3416</td><td>5152</td><td>gnl|PID|d100974</td><td>unknown [Bacillus subtilis]</td><td>50</td><td>27</td><td>1737</td></tr>
<tr><td>51</td><td>7</td><td>4000</td><td>5181</td><td>gi|1592027</td><td>carbamoyl-phosphate synthase, pyrimidine-specific, large subunit [Methanococcus jannaschii]</td><td>50</td><td>27</td><td>1182</td></tr>
<tr><td>51</td><td>9</td><td>7179</td><td>8303</td><td>gi|1591847</td><td>type I restriction-modification enzyme, S subunit [Methanococcus jannaschii]</td><td>50</td><td>28</td><td>1125</td></tr>
<tr><td>52</td><td>8</td><td>8740</td><td>9534</td><td>gi|144297</td><td>acetyl esterase (XynC) [Caldocellum saccharolyticum]</td><td>50</td><td>34</td><td>795</td></tr>
<tr><td>52</td><td>16</td><td>16591</td><td>15770</td><td>gi|2108229</td><td>basic surface protein [Lactobacillus fermentum]</td><td>50</td><td>34</td><td>822</td></tr>
<tr><td>57</td><td>7</td><td>6031</td><td>6336</td><td>gi|2275264</td><td>60S ribosomal protein L7B [Schizosaccharomyces pombe]</td><td>50</td><td>40</td><td>306</td></tr>
<tr><td>71</td><td>23</td><td>29348</td><td>28383</td><td>gnl|PID|d101328</td><td>YqjA [Bacillus subtilis]</td><td>50</td><td>30</td><td>966</td></tr>
<tr><td>86</td><td>12</td><td>11155</td><td>10769</td><td>gnl|PID|e324964</td><td>hypothetical protein [Bacillus subtilis]</td><td>50</td><td>24</td><td>387</td></tr>
<tr><td>93</td><td>2</td><td>1205</td><td>330</td><td>gi|1066016</td><td>similar to Escherichia coli pyruvate, water dikinase, Swiss-Prot Accession Number P23538 [Pyrococcus furiosus]</td><td>50</td><td>24</td><td>876</td></tr>
<tr><td>96</td><td>5</td><td>1673</td><td>2959</td><td>gnl|PID|e322433</td><td>gamma-glutamylcysteine synthetase [Brassica juncea]</td><td>50</td><td>29</td><td>1287</td></tr>
<tr><td>98</td><td>2</td><td>218</td><td>1171</td><td>gi|151110</td><td>leucine-, isoleucine-, and valine-binding protein [Pseudomonas aeruginosa]</td><td>50</td><td>30</td><td>954</td></tr>
<tr><td>103</td><td>4</td><td>3303</td><td>2785</td><td>gi|154330</td><td>O-antigen ligase [Salmonella typhimurium]</td><td>50</td><td>31</td><td>519</td></tr>
<tr><td>115</td><td>5</td><td>6480</td><td>5980</td><td>gi|895747</td><td>putative cel operon regulator [Bacillus subtilis]</td><td>50</td><td>26</td><td>501</td></tr>
<tr><td>129</td><td>11</td><td>7559</td><td>7305</td><td>gi|1216475</td><td>skeletal muscle ryanodine receptor [Homo sapiens]</td><td>50</td><td>32</td><td>255</td></tr>
<tr><td>129</td><td>13</td><td>8192</td><td>7965</td><td>gi|152271</td><td>319-kDA protein [Rhizobium meliloti]</td><td>50</td><td>30</td><td>228</td></tr>
<tr><td>151</td><td>5</td><td>7634</td><td>6819</td><td>gi|40348</td><td>put. resolvase Tnp I (AA 1 - 284) [Bacillus thuringiensis]</td><td>50</td><td>35</td><td>816</td></tr>
<tr><td>153</td><td>1</td><td>1</td><td>597</td><td>gnl|PID|d102015</td><td>(AB001488) SIMILAR TO NITROREDUCTASE. [Bacillus subtilis]</td><td>50</td><td>29</td><td>597</td></tr>
</table>

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

<table>
<tr><th>Contig ID</th><th>ORF ID</th><th>Start (nt)</th><th>Stop (nt)</th><th>match acession</th><th>match gene name</th><th>% sim</th><th>% ident</th><th>length (nt)</th></tr>
<tr><td>155</td><td>5</td><td>5986</td><td>5432</td><td>gi|1276880</td><td>EpsG [Streptococcus thermophilus]</td><td>50</td><td>28</td><td>555</td></tr>
<tr><td>160</td><td>9</td><td>7390</td><td>6323</td><td>gi|1786983</td><td>(AE000179) o331; 92 pct identical to the 333 aa hypothetical protein YBHE_ECOLI SW: P52697; 26 pct identical (7 gaps) to 167 residues of the 373 aa protein MLE_TRICU SW: P46057; SW: P52697 [Escherichia coli]</td><td>50</td><td>30</td><td>1068</td></tr>
<tr><td>163</td><td>6</td><td>7396</td><td>8091</td><td>gnl|PID|d101313</td><td>YqeN [Bacillus subtilis]</td><td>50</td><td>22</td><td>696</td></tr>
<tr><td>167</td><td>6</td><td>5232</td><td>3940</td><td>gi|413926</td><td>ipa-2r gene product [Bacillus subtilis]</td><td>50</td><td>27</td><td>1293</td></tr>
<tr><td>169</td><td>2</td><td>807</td><td>130</td><td>gnl|PID|e304540</td><td>endolysin [Bacteriophage Bastille]</td><td>50</td><td>35</td><td>678</td></tr>
<tr><td>171</td><td>5</td><td>3168</td><td>4025</td><td>gi|606080</td><td>ORF_o290; Geneplot suggests frameshift linking to o267, not found [Escherichia coli]</td><td>50</td><td>27</td><td>858</td></tr>
<tr><td>210</td><td>11</td><td>8151</td><td>8414</td><td>gi|330038</td><td>HRV 2 polyprotein [Human rhinovirus]</td><td>50</td><td>25</td><td>264</td></tr>
<tr><td>364</td><td>1</td><td>1538</td><td>135</td><td>gi|393396</td><td>Tb-292 membrane associated protein [Trypanosoma brucei subgroup]</td><td>50</td><td>31</td><td>1404</td></tr>
<tr><td>10</td><td>7</td><td>5911</td><td>5090</td><td>gi|144859</td><td>ORF B [Clostridium perfringens]</td><td>49</td><td>24</td><td>822</td></tr>
<tr><td>26</td><td>5</td><td>10754</td><td>9768</td><td>gi|142440</td><td>ATP-dependent nuclease [Bacillus subtilis]</td><td>49</td><td>31</td><td>987</td></tr>
<tr><td>66</td><td>7</td><td>9777</td><td>8398</td><td>gi|414170</td><td>trkA gene product [Methanosarcina mazeii]</td><td>49</td><td>26</td><td>1380</td></tr>
<tr><td>77</td><td>6</td><td>5364</td><td>4648</td><td>gnl|PID|e285322</td><td>RecX protein [Mycobacterium smegmatis]</td><td>49</td><td>28</td><td>717</td></tr>
<tr><td>82</td><td>13</td><td>12689</td><td>13249</td><td>gnl|PID|e255091</td><td>hypothetical protein [Bacillus subtilis]</td><td>49</td><td>20</td><td>561</td></tr>
<tr><td>93</td><td>9</td><td>4866</td><td>4531</td><td>gi|40067</td><td>X gene product [Bacillus sphaericus]</td><td>49</td><td>26</td><td>336</td></tr>
<tr><td>112</td><td>5</td><td>4019</td><td>4948</td><td>gi|1574380</td><td>lic-1 operon protein (licB) [Haemophilus influenzae]</td><td>49</td><td>27</td><td>930</td></tr>
<tr><td>129</td><td>7</td><td>6058</td><td>4949</td><td>gnl|PID|e267587</td><td>Unknown [Bacillus subtilis]</td><td>49</td><td>35</td><td>1110</td></tr>
<tr><td>135</td><td>5</td><td>3875</td><td>4438</td><td>gi|39573</td><td>P20 (AA 1-178) [Bacillus licheniformis]</td><td>49</td><td>25</td><td>564</td></tr>
<tr><td>154</td><td>2</td><td>1423</td><td>1953</td><td>gnl|PID|d101102</td><td>regulatory components of sensory transduction system [Synechocystis sp.]</td><td>49</td><td>29</td><td>531</td></tr>
<tr><td>156</td><td>5</td><td>2878</td><td>1637</td><td>gnl|PID|d101732</td><td>hypothetical protein [Synechocystis sp.]</td><td>49</td><td>25</td><td>1242</td></tr>
<tr><td>173</td><td>5</td><td>3500</td><td>2940</td><td>gi|490324</td><td>LORF X gene product [unidentified]</td><td>49</td><td>30</td><td>561</td></tr>
<tr><td>182</td><td>1</td><td>1057</td><td>2</td><td>gi|331002</td><td>first methionine codon in the ECLF1 ORF [Saimiriine herpesvirus 2]</td><td>49</td><td>25</td><td>1056</td></tr>
<tr><td>192</td><td>6</td><td>5352</td><td>3667</td><td>gi|2394472</td><td>(AF024499) contains similarity to homeobox domains [Caenorhabditis elegans]</td><td>49</td><td>23</td><td>1686</td></tr>
<tr><td>253</td><td>4</td><td>1129</td><td>1350</td><td>gi|531116</td><td>SIR4 protein [Saccharomyces cerevisiae]</td><td>49</td><td>23</td><td>222</td></tr>
<tr><td>277</td><td>1</td><td>600</td><td>136</td><td>gi|396844</td><td>ORF (18 kDa) [Vibrio cholerae]</td><td>49</td><td>32</td><td>465</td></tr>
<tr><td>327</td><td>3</td><td>1435</td><td>887</td><td>gi|733524</td><td>phosphatidylinositol-4,5-diphosphate 3-kinase [Dictyostelium discoideum]</td><td>49</td><td>24</td><td>549</td></tr>
</table>

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

<table>
<tr><th>Contig ID</th><th>ORF ID</th><th>Start (nt)</th><th>Stop (nt)</th><th>match acession</th><th>match gene name</th><th>% sim</th><th>% ident</th><th>length (nt)</th></tr>
<tr><td>365</td><td>3</td><td>1436</td><td>132</td><td>gi|393394</td><td>Tb-291 membrane associated protein [Trypanosoma brucei subgroup]</td><td>49</td><td>31</td><td>1305</td></tr>
<tr><td>33</td><td>7</td><td>4461</td><td>3277</td><td>gi|145644</td><td>codes for a protein of unknown function [Escherichia coli]</td><td>48</td><td>26</td><td>1185</td></tr>
<tr><td>40</td><td>2</td><td>652</td><td>1776</td><td>gnl|PID|e290649</td><td>ornithine decarboxylase [Nicotiana tabacum]</td><td>48</td><td>29</td><td>1125</td></tr>
<tr><td>67</td><td>4</td><td>1377</td><td>2384</td><td>gi|1772652</td><td>2-keto-3-deoxygluconate kinase [Haloferax alicantei]</td><td>48</td><td>30</td><td>1008</td></tr>
<tr><td>74</td><td>2</td><td>4269</td><td>3871</td><td>gi|2182678</td><td>(AE000101) Y4vJ [Rhizobium sp. NGR234]</td><td>48</td><td>27</td><td>399</td></tr>
<tr><td>81</td><td>2</td><td>1326</td><td>541</td><td>gi|153672</td><td>lactose repressor [Streptococcus mutans]</td><td>48</td><td>33</td><td>786</td></tr>
<tr><td>81</td><td>4</td><td>2981</td><td>3646</td><td>gi|146042</td><td>fuculose-1-phosphate aldolase (fucA) [Escherichia coli]</td><td>48</td><td>30</td><td>666</td></tr>
<tr><td>97</td><td>1</td><td>602</td><td>51</td><td>gi|153794</td><td>rgg [Streptococcus gordonii]</td><td>48</td><td>29</td><td>552</td></tr>
<tr><td>110</td><td>1</td><td>1</td><td>3132</td><td>gi|1381114</td><td>prtB gene product [Lactobacillus delbrueckii]</td><td>48</td><td>23</td><td>3132</td></tr>
<tr><td>131</td><td>5</td><td>2914</td><td>2147</td><td>gnl|PID|e183811</td><td>Acyl-ACP thioesterase [Brassica napus]</td><td>48</td><td>27</td><td>768</td></tr>
<tr><td>133</td><td>4</td><td>3494</td><td>2628</td><td>gnl|PID|e261988</td><td>putative ORF [Bacillus subtilis]</td><td>48</td><td>27</td><td>867</td></tr>
<tr><td>139</td><td>6</td><td>4231</td><td>4599</td><td>gi|1049388</td><td>ZK470.1 gene product [Caenorhabditis elegans]</td><td>48</td><td>23</td><td>369</td></tr>
<tr><td>139</td><td>8</td><td>5036</td><td>5665</td><td>gi|1022725</td><td>unknown [Staphylococcus haemolyticus]</td><td>48</td><td>29</td><td>630</td></tr>
<tr><td>140</td><td>12</td><td>11936</td><td>11007</td><td>gnl|PID|d102049</td><td>H. influenzae, ribosomal protein alanine acetyltransferase; P44305 (189) [Bacillus subtilis]</td><td>48</td><td>27</td><td>930</td></tr>
<tr><td>146</td><td>9</td><td>5670</td><td>4654</td><td>gi|1591731</td><td>melvalonate kinase [Methanococcus jannaschii]</td><td>48</td><td>24</td><td>1017</td></tr>
<tr><td>161</td><td>3</td><td>1280</td><td>2374</td><td>gnl|PID|d101578</td><td>Collagenase precursor (EC 3.4.-.-). [Escherichia coli]</td><td>48</td><td>24</td><td>1095</td></tr>
<tr><td>172</td><td>11</td><td>10581</td><td>11048</td><td>gnl|PID|d101132</td><td>hypothetical protein [Synechocystis sp.]</td><td>48</td><td>27</td><td>468</td></tr>
<tr><td>182</td><td>4</td><td>2930</td><td>2586</td><td>gi|40067</td><td>X gene product [Bacillus sphaericus]</td><td>48</td><td>37</td><td>345</td></tr>
<tr><td>210</td><td>15</td><td>10786</td><td>11196</td><td>sp|P13940|LE29_</td><td>LATE EMBRYOGENESIS ABUNDANT PROTEIN D-29 (LEA D-29).</td><td>48</td><td>30</td><td>411</td></tr>
<tr><td>214</td><td>12</td><td>6231</td><td>6482</td><td>gi|40389</td><td>non-toxic components [Clostridium botulinum]</td><td>48</td><td>26</td><td>252</td></tr>
<tr><td>221</td><td>1</td><td>704</td><td>3</td><td>gi|1573364</td><td>H. influenzae predicted coding region HI0392 [Haemophilus influenzae]</td><td>48</td><td>27</td><td>702</td></tr>
<tr><td>227</td><td>2</td><td>647</td><td>3928</td><td>gi|1673693</td><td>(AE000005) Mycoplasma pneumoniae, C09_orf718 Protein [Mycoplasma pneumoniae]</td><td>48</td><td>30</td><td>3282</td></tr>
<tr><td>253</td><td>2</td><td>480</td><td>758</td><td>gnl|PID|e236697</td><td>unknown [Saccharomyces cerevisiae]</td><td>48</td><td>31</td><td>279</td></tr>
<tr><td>363</td><td>3</td><td>1874</td><td>1122</td><td>gi|18137</td><td>cgcr-4 product [Chlamydomonas reinhardtii]</td><td>48</td><td>40</td><td>753</td></tr>
<tr><td>389</td><td>1</td><td>505</td><td>2</td><td>gi|18137</td><td>cgcr-4 product [Chlamydomonas reinhardtii]</td><td>48</td><td>38</td><td>504</td></tr>
<tr><td>3</td><td>21</td><td>20879</td><td>22258</td><td>gnl|PID|e264778</td><td>putative maltose-binding pootein [Streptomyces coelicolor]</td><td>47</td><td>33</td><td>1380</td></tr>
</table>

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

<table>
<tr><th>Contig ID</th><th>ORF ID</th><th>Start (nt)</th><th>Stop (nt)</th><th>match acession</th><th>match gene name</th><th>% sim</th><th>% ident</th><th>length (nt)</th></tr>
<tr><td>6</td><td>4</td><td>4089</td><td>4658</td><td>gi|39573</td><td>P20 (AA 1-178) [Bacillus licheniformis]</td><td>47</td><td>23</td><td>570</td></tr>
<tr><td>15</td><td>3</td><td>3736</td><td>1760</td><td>gnl|PID|d100572</td><td>unknown [Bacillus subtilis]</td><td>47</td><td>25</td><td>1977</td></tr>
<tr><td>35</td><td>15</td><td>14516</td><td>13263</td><td>gi|1773351</td><td>Cap5L [Staphylococcus aureus]</td><td>47</td><td>20</td><td>1254</td></tr>
<tr><td>51</td><td>6</td><td>3547</td><td>4002</td><td>pir|A37024|A370</td><td>32K antigen precursor - Mycobacterium tuberculosis</td><td>47</td><td>38</td><td>456</td></tr>
<tr><td>55</td><td>8</td><td>10154</td><td>9273</td><td>gi|39848</td><td>U3 [Bacillus subtilis]</td><td>47</td><td>26</td><td>882</td></tr>
<tr><td>92</td><td>4</td><td>1753</td><td>3276</td><td>gnl|PID|e280611</td><td>PCPC [Streptococcus pneumoniae]</td><td>47</td><td>35</td><td>1524</td></tr>
<tr><td>127</td><td>9</td><td>5589</td><td>5386</td><td>gi|1786458</td><td>(AE000134) f120; This 120 aa orf is 76 pct identical (0 gaps) to 42 residues of an approx. 48 aa protein Y127_HAEIN SW: P43949 [Escherichia coli]</td><td>47</td><td>32</td><td>204</td></tr>
<tr><td>130</td><td>2</td><td>1232</td><td>1759</td><td>gnl|PID|e266555</td><td>unknown [Mycobacterium tuberculosis]</td><td>47</td><td>23</td><td>528</td></tr>
<tr><td>140</td><td>4</td><td>4951</td><td>3542</td><td>gnl|PID|d100964</td><td>homologue of hypothetical protein in a rapamycin synthesis gene cluster of Streptomyces hygroscopicus [Bacillus subtilis]</td><td>47</td><td>24</td><td>1410</td></tr>
<tr><td>151</td><td>4</td><td>6814</td><td>6200</td><td>gi|1522674</td><td>M. jannaschii predicted coding region MJECL41 [Methanococcus jannaschii]</td><td>47</td><td>27</td><td>615</td></tr>
<tr><td>157</td><td>3</td><td>803</td><td>1174</td><td>gnl|PID|d101320</td><td>YqgZ [Bacillus subtilis]</td><td>47</td><td>25</td><td>372</td></tr>
<tr><td>178</td><td>5</td><td>3267</td><td>2155</td><td>gi|2367190</td><td>(AE000390) o334; sequence change joins ORFs ygjR & ygjS from earlier version (YGJR_ECOLI SW: P42599 and YGJS_ECOLI SW: P42600) [Escherichia coli]</td><td>47</td><td>30</td><td>1113</td></tr>
<tr><td>273</td><td>1</td><td>2</td><td>1549</td><td>gnl|PID|e254973</td><td>autolysin sensor kinase [Bacillus subtilis]</td><td>47</td><td>32</td><td>1548</td></tr>
<tr><td>300</td><td>2</td><td>880</td><td>644</td><td>gi|1835755</td><td>zinc finger protein Png-1 [Mus musculus]</td><td>47</td><td>22</td><td>237</td></tr>
<tr><td>54</td><td>14</td><td>14182</td><td>12638</td><td>pir|S43609|S436</td><td>rofA protein - Streptococcus pyogenes</td><td>46</td><td>24</td><td>1545</td></tr>
<tr><td>88</td><td>1</td><td>2</td><td>1018</td><td>gnl|PID|e223891</td><td>xylose repressor [Anaerocellum thermophilum]</td><td>46</td><td>27</td><td>1017</td></tr>
<tr><td>96</td><td>7</td><td>4553</td><td>5860</td><td>gnl|PID|d101652</td><td>ORF_ID:o347#5; similar to [SwissProt Accession Number P45272] [Escherichia coli]</td><td>46</td><td>23</td><td>1308</td></tr>
<tr><td>112</td><td>1</td><td>1127</td><td>3</td><td>gi|2209215</td><td>(AF004325) putative oligosaccharide repeat unit transporter [Streptococcus pneumoniae]</td><td>46</td><td>24</td><td>1125</td></tr>
<tr><td>122</td><td>13</td><td>7308</td><td>7982</td><td>gi|1054776</td><td>hr44 gene product [Homo sapiens]</td><td>46</td><td>34</td><td>675</td></tr>
<tr><td>127</td><td>14</td><td>9198</td><td>8125</td><td>gi|1469286</td><td>afuA gene product [Actinobacillus pleuropneumoniae]</td><td>46</td><td>28</td><td>1074</td></tr>
<tr><td>132</td><td>4</td><td>7093</td><td>6197</td><td>gi|153794</td><td>rgg [Streptococcus gordonii]</td><td>46</td><td>26</td><td>897</td></tr>
<tr><td>140</td><td>8</td><td>8220</td><td>7723</td><td>gi|1235795</td><td>pullulanase [Thermoanaerobacterium thermosulfurigenes]</td><td>46</td><td>21</td><td>498</td></tr>
<tr><td>140</td><td>9</td><td>9205</td><td>8315</td><td>gi|407878</td><td>leucine rich protein [Streptococcus equisimilis]</td><td>46</td><td>27</td><td>891</td></tr>
</table>

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

<table>
<tr><th>Contig ID</th><th>ORF ID</th><th>Start (nt)</th><th>Stop (nt)</th><th>match acession</th><th>match gene name</th><th>% sim</th><th>% ident</th><th>length (nt)</th></tr>
<tr><td>162</td><td>1</td><td>1</td><td>1125</td><td>gi|1143209</td><td>ORF7; Method: conceptual translation supplied by author [Shigella sonnei]</td><td>46</td><td>25</td><td>1125</td></tr>
<tr><td>199</td><td>1</td><td>1</td><td>585</td><td>gi|1947171</td><td>(AF000299) No definition line found [Caenorhabditis elegans]</td><td>46</td><td>28</td><td>585</td></tr>
<tr><td>223</td><td>3</td><td>1971</td><td>1477</td><td>sp|P02562|MYSS_</td><td>MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (FRAGMENTS).</td><td>46</td><td>27</td><td>495</td></tr>
<tr><td>232</td><td>2</td><td>760</td><td>1608</td><td>gi|1016112</td><td>ycf38 gene product [Cyanophora paradoxa]</td><td>46</td><td>28</td><td>849</td></tr>
<tr><td>292</td><td>1</td><td>687</td><td>220</td><td>gi|1673744</td><td>(AE000011) Mycoplasma pneumoniae, cytidine deaminase; similar to GenBank Accession Number C53312, from M. pirum [Mycoplasma pneumoniae]</td><td>46</td><td>29</td><td>468</td></tr>
<tr><td>30</td><td>8</td><td>5843</td><td>6472</td><td>gi|1788049</td><td>(AE000270) o235; This 235 aa orf is 29 pct identical (10 gaps) to 198 residues of an approx. 216 aa protein YTXB_BACSU SW: P06568 [Escherichia coli]</td><td>45</td><td>24</td><td>630</td></tr>
<tr><td>48</td><td>6</td><td>3461</td><td>3868</td><td>gi|722339</td><td>unknown [Acetobacter xylinum]</td><td>45</td><td>29</td><td>408</td></tr>
<tr><td>60</td><td>1</td><td>307</td><td>2</td><td>gi|1699079</td><td>coded for by C. elegans cDNA yk41h4.3; coded for by C. elegans cDNA yk148g10.5; coded for by C. elegans cDNA yk152g5.5; coded for by C. elegans cDNA yk59a10.5; coded for by C. elegans cDNA yk41h4.5; coded for by C. elegans cDNA cm20g10; coded</td><td>45</td><td>36</td><td>306</td></tr>
<tr><td>72</td><td>16</td><td>14371</td><td>14874</td><td>gi|1321900</td><td>NADH dehydrogenase (ubiquinone) [Artemia franciscana]</td><td>45</td><td>25</td><td>504</td></tr>
<tr><td>99</td><td>7</td><td>9158</td><td>7941</td><td>gi|152192</td><td>mutation causes a succinoglucan-minus phenotype; ExoQ is atransmembrane protein; third gene of the exoYFQ operon;; putative [Rhizobium meliloti]</td><td>45</td><td>28</td><td>1218</td></tr>
<tr><td>127</td><td>12</td><td>7046</td><td>6606</td><td>bbs|153689</td><td>HitB=iron utilization protein [Haemophilus influenzae, type b, DL42, NTHI TN106, Peptide, 506 aa] [Haemophilus influenzae]</td><td>45</td><td>24</td><td>441</td></tr>
<tr><td>137</td><td>5</td><td>1561</td><td>2619</td><td>gi|472921</td><td>v-type Na-ATPase [Enterococcus hirae]</td><td>45</td><td>33</td><td>1059</td></tr>
<tr><td>209</td><td>1</td><td>774</td><td>364</td><td>gi|304141</td><td>restriction endonuclease beta subunit [Bacillus coagulans]</td><td>45</td><td>28</td><td>411</td></tr>
<tr><td>314</td><td>1</td><td>604</td><td>2</td><td>gi|1480457</td><td>latex allergen [Hevea brasiliensis]</td><td>45</td><td>31</td><td>603</td></tr>
<tr><td>20</td><td>18</td><td>19782</td><td>20288</td><td>gi|433942</td><td>ORF [Lactococcus lactis]</td><td>44</td><td>26</td><td>507</td></tr>
<tr><td>87</td><td>8</td><td>7030</td><td>6452</td><td>gi|537207</td><td>ORF_f277 [Escherichia coli]</td><td>44</td><td>26</td><td>579</td></tr>
<tr><td>166</td><td>5</td><td>4909</td><td>4037</td><td>gnl|PID|e308082</td><td>membrane transport protein [Bacillus subtilis]</td><td>44</td><td>25</td><td>873</td></tr>
<tr><td>247</td><td>1</td><td>818</td><td>75</td><td>gnl|PID|d100718</td><td>ORF1 [Bacillus sp.]</td><td>44</td><td>20</td><td>744</td></tr>
<tr><td>32</td><td>3</td><td>1885</td><td>3876</td><td>gi|2351768</td><td>PspA [Streptococcus pneumoniae]</td><td>43</td><td>24</td><td>1992</td></tr>
<tr><td>36</td><td>17</td><td>15467</td><td>18256</td><td>gi|1045739</td><td>M. genitalium predicted coding region MG064 [Mycoplasma genitalium]</td><td>43</td><td>26</td><td>2790</td></tr>
<tr><td>54</td><td>15</td><td>14656</td><td>17343</td><td>gi|520541</td><td>penicillin-binding proteins 1A and 1B [Bacillus subtilis]</td><td>43</td><td>27</td><td>2688</td></tr>
<tr><td>67</td><td>2</td><td>696</td><td>1352</td><td>gi|536934</td><td>yjcA gene product [Escherichia coli]</td><td>43</td><td>29</td><td>657</td></tr>
<tr><td>139</td><td>2</td><td>2416</td><td>338</td><td>gi|396400</td><td>similar to eukaryotic Na+/H+ exchangers [Escherichia coli]</td><td>43</td><td>24</td><td>2079</td></tr>
</table>

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
298	1	3	809	gi|413972	ipa-48r gene product [Bacillus subtilis]	43	24	807
387	1	47	427	gi|2315652	(AF016669) No definition line found [Caenorhabditis elegans]	43	30	381
185	4	4221	3127	gi|2182399	(AE000073) Y4fP [Rhizobium sp. NGR234]	41	25	1095
340	1	582	70	gnl|PID|e218681	CDP-diacylglycerol synthetase [Arabidopsis thaliana]	41	20	513
363	6	4205	1914	gi|1256742	R27-2 protein [Trypanosoma cruzi]	41	27	2292
368	2	2	943	gi|21783	LMW glutenin (AA 1-356) [Triticum aestivum]	41	34	942
155	3	4489	2861	gi|42023	member of ATP-dependent transport family, very similar to mdr proteins and hemolysin B, export protein [Escherichia coli]	40	18	1629
365	2	95	1438	gi|1633572	Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]	40	21	1344
1	3	2979	3860	gnl|PID|d101908	hypothetical protein [Synechocystis sp.]	39	26	882
1	5	3814	4647	gnl|PID|d101961	hypothetical protein [Synechocystis sp.]	39	19	834
26	6	14035	10724	gi|142439	ATP-dependent nuclease [Bacillus subtilis]	38	20	3312
47	1	3	4916	gi|632549	NF-180 [Petromyzon marinus]	36	23	4914

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
1	4	3428	3009
1	6	4611	4964
3	2	818	994
3	3	1182	1574
3	7	5382	6497
3	25	25046	25396
3	26	25625	26317
6	2	1519	1689
6	14	12875	12618
6	15	13215	12841
6	18	15977	15390
7	12	9955	9419
7	13	10161	9910
8	6	3915	4280
9	9	6024	5704
10	8	6909	6298
10	9	7136	6888
10	11	7968	7672
12	1	1140	4
12	3	1779	1456
14	2	1913	1434
16	1	1	243
16	5	5675	3087
17	1	324	34
17	3	1451	1050
17	9	4890	4465
20	14	14544	15893

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
21	3	3359	2589
21	5	4802	4482
22	21	17099	17362
22	25	19467	19982
22	33	25540	25764
22	35	26388	26218
22	36	26382	27572
23	7	6655	6032
23	8	7132	6653
24	1	36	518
25	5	3009	2641
27	4	4819	4223
27	5	4789	4956
28	5	3017	1797
28	8	4272	3850
28	10	5028	4597
28	11	5746	5072
29	7	5596	4919
29	8	5039	5518
29	9	5595	8207
30	9	6511	6263
31	6	2664	2344
32	5	5203	5538
33	8	5327	4668
34	10	8024	7740
34	12	9360	8641
34	13	9667	9377

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
34	18	13104	11902
35	11	9688	8588
35	12	11073	9670
36	2	334	1041
36	12	11120	10893
36	13	10993	11388
36	15	12172	14595
38	7	4269	4577
38	8	4480	5001
38	10	5517	5711
38	17	10732	11376
40	3	1728	3143
43	1	172	5
43	7	8884	8732
43	8	9568	9071
44	4	4831	6831
45	3	3204	3665
46	4	3875	3468
46	7	6074	7081
48	5	3196	3582
48	8	4579	4229
48	11	9323	8922
48	16	13042	12494
48	20	16342	15764
48	24	17971	18351
48	30	21979	21776
49	1	209	3

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
50	4	3307	2672
51	5	3239	3598
52	11	12146	12883
54	7	5588	5187
54	8	6013	5459
54	9	6004	6210
54	16	17685	17506
55	9	10515	10123
55	12	11947	12141
56	3	935	1387
56	4	1496	1939
57	3	1624	2130
57	4	2100	2501
58	6	7541	7335
59	1	2	430
59	4	2416	2736
59	5	2734	3063
59	8	4743	5549
59	9	5459	5929
60	6	5741	6451
61	3	2395	1772
61	5	3316	3176
64	1	2722	2
66	2	1180	3147
66	8	9082	9495
67	3	1343	1182
69	2	1165	980

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
70	5	4059	3922
70	6	4215	4057
70	9	5268	5504
71	15	20351	21901
71	16	21859	22338
71	19	26204	27556
72	9	8458	8081
73	4	3815	4216
73	6	4214	4582
73	7	4369	4773
73	10	7183	6428
73	15	9462	9668
76	1	524	195
76	2	867	535
76	11	8602	9210
80	6	7924	8109
81	1	244	2
81	10	6631	8931
83	4	1872	1150
83	17	16810	16460
84	3	4464	2929
86	2	2147	1092
86	4	3606	2875
86	19	16767	17114
87	5	5326	5000
87	7	6459	6001
87	9	7224	7006

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
87	18	17930	17670
87	19	18275	17928
88	2	1619	1840
88	4	2711	2878
88	9	6252	6016
89	3	2634	1621
89	9	7371	6868
90	2	899	2395
90	3	1143	952
91	3	2959	3141
91	4	3170	3691
91	6	4253	4573
93	1	391	2
93	6	2648	2379
93	8	4533	3712
96	1	3	182
96	2	904	632
96	3	1407	1147
96	4	1250	1420
97	9	7043	6753
99	15	18522	18692
99	17	19717	19541
100	2	4094	1980
103	1	48	299
103	6	4924	4373
104	5	6142	6735
105	7	6098	6517

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
106	1	1	363
106	10	9832	10212
108	1	2	268
111	3	3417	3788
111	4	3809	4606
115	10	10854	10438
116	3	2873	2121
118	2	2274	1357
122	4	2698	2333
122	10	5858	6199
122	12	6301	7416
124	2	346	690
128	4	2544	3368
129	1	689	102
129	2	1011	724
129	8	6454	6056
129	9	6540	6277
129	12	7809	7621
131	3	1433	756
131	10	5972	5673
134	11	11838	11209
135	2	625	1140
136	4	2913	3830
137	2	325	134
139	12	14027	14521
139	13	14840	14532
139	14	15363	14875

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
140	20	19822	20838
142	1	1	285
146	3	760	479
146	4	1149	778
146	7	3604	2885
146	13	8223	9401
146	14	9399	10676
146	15	10052	9750
147	7	7488	7276
147	9	8913	8647
148	7	5298	4765
149	1	2	1936
149	3	2557	2880
149	9	6258	6070
150	2	1355	579
150	3	2556	1909
153	3	2061	2642
154	3	1953	1741
155	2	2181	1411
156	8	4550	4311
157	1	37	294
159	2	631	780
159	4	1384	1722
159	7	3271	4017
161	2	1332	1018
165	3	5535	4945
166	6	5406	4972

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
167	9	6075	6395
169	5	2828	3205
170	7	6485	6243
170	8	6964	6362
170	9	7303	6962
170	11	8790	7906
171	9	7150	7476
172	5	2298	1948
173	4	2913	2677
175	2	659	835
175	3	893	1789
176	2	1487	546
176	3	2200	1466
177	9	4686	4925
177	10	4923	5177
177	11	5111	5347
177	13	7396	8703
178	6	3452	3724
181	5	1853	2473
182	2	2112	1102
182	3	2617	2006
183	2	2126	2320
185	5	4683	4219
185	6	4846	4634
187	4	2940	3557
188	4	3686	4363
188	5	4183	4821

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
188	6	5882	6493
189	5	3143	2844
189	9	5956	5564
191	1	618	4
191	11	10357	10001
192	3	2861	2268
192	4	3081	2878
192	7	6800	5331
193	3	997	839
194	4	2315	2127
195	5	6249	4543
195	6	6620	6231
196	2	1553	1849
197	1	1	861
198	9	6844	6644
200	5	5329	5769
200	6	5993	6595
204	5	3914	3276
205	2	447	1709
209	4	2038	2460
209	5	2458	2682
210	10	7370	8230
210	13	9029	10441
210	14	10439	10705
214	5	2581	2330
214	9	5065	5277
214	11	5996	5754

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
217	2	541	194
218	2	914	1432
218	3	1430	1972
218	6	3639	3821
219	1	458	39
220	1	869	600
223	4	2617	1964
227	1	1	510
234	4	1539	1312
234	6	2116	1838
235	1	52	312
235	2	310	687
238	1	660	64
246	1	1	270
248	1	3	362
248	2	443	1222
254	3	2789	792
258	2	1179	1616
260	3	1770	2123
263	1	653	177
263	4	2244	1900
263	5	3569	2973
266	1	1	342
266	2	177	1022
270	2	1124	1681
272	1	857	186
275	2	1684	2295

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
278	1	2	406
282	1	714	391
282	4	1463	1134
287	2	1119	826
288	1	540	4
289	1	684	4
291	5	1589	1858
293	2	2539	2925
294	1	21	608
296	2	494	700
296	3	670	843
302	1	261	530
309	3	559	350
310	2	249	1889
316	2	2087	1818
317	2	1048	584
318	2	313	777
319	3	477	133
327	2	912	607
331	1	1	549
333	1	2	535
333	2	465	82
333	3	127	342
341	1	1	705
345	2	895	701
346	2	750	199
349	1	1	198

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
350	2	81	413
355	1	44	973
358	2	636	448
360	2	948	628
364	2	1639	1265
378	1	345	1004
379	2	683	510
381	1	109	693
385	1	150	4
385	2	269	30

(1) GENERAL INFORMATION:

(i) APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
Brian A. Dougherty

(ii) TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences

(iii) NUMBER OF SEQUENCES: 391

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Human Genome Sciences, Inc.

(B) STREET: 9410 Key West Avenue

(C) CITY: Rockville

(D) STATE: Maryland

(E) COUNTRY: USA

(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

(B) COMPUTER: HP Vectra 486/33

(C) OPERATING SYSTEM: MSDOS version 6.2

(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Brookes, A. Anders

(B) REGISTRATION NUMBER: 36,373

(C) REFERENCE/DOCKET NUMBER: PB340P1

(vi) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (301) 309-8504

(B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5625 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCAAGCAAAA CCAGCTACAG CTAAAGGAAC TTACGTAACA AACTTGACTA TCACAACTAC 60

TCAAGGTGTT GGTATCAAAG TTGACGTAAA CTCACTTTAA TCAGTAGTTA AAGTAATGTA 120

AAAAAGTTGA AGACGCTATG TCTCAACTTT TTTTGATGTA CGACGGGCAT GTTGTATAGT 180

AGATGTGTAC TATTCTAGTT TCAATCTACT ATAGTAGCTC AGAAGTCGGT ACTTAAACGT 240

GCTATATCAA AACCAGTCCT TGAAAAACGT GGACTGGTTT CGTGTTTGGA TTATTACCTT 300

GAACGACATG CGTTAAAAGT TAGTTGAACC GCCGTATGCC GAACGGACGT ACGGTGGTGT 360

GAGAGGGGCT AGAGATTATC CCCTACTCGA TTTCGAAATC TAGTGGAATG AATCTGGAAT 420

AGTCCATCGA GCTTTCTAAT ACTCTTCGAA AATCTCTTCA AACCACGTCA ACGTCGCCTT 480

GCCGTGCGTA TGGTTACTGA CTTCGTCAGT TCTATCCACA ACCTCAAAAC AGTGTTTTGA 540

GCTGACTACG TCAGTTCCAT CTACAACCTC AAAACAGTGT TTTGAGCAAC CTGCGGCTAG 600

TTTCCTAGTT TGCTCTTTGG TTTTCATTGA GTATAACACA TTGTTAGAAG TTGGTTTAAA 660

TTTCCTAATC AGTTTGTTCA CATTTACCTT CGATATATTA TATCCCATAG TTAAGGTTGG 720

TCATACAGAT GATTATAGTC ATGGAGCCGT AAAACTTAGT GTTTCTTTAG TTGACAAAGA 780

TGCCATGAAA AAAATATTTG TAACTGTAAT AGGATATTTT GAAATAAATA TAGATGAAAA 840

TATCACCGAT ATTCTATACG TAAATGGTAC TGCTATTCTT TATCTTTATT TACGTTCAAT 900

TGTTTCAATA GTTTCGGCAA TTGATAGCAG TGAAGCAATG TTGCTACCTA TCATTAATGT 960

TTTAGAGTTA CTAGATAAAT CTCAACCTTT TGAAGAAGAA TAATTTATTA GCTCACTAAA 1020

TTGAGGGTAA GGAAAAGTAA AAGCAGTAAG AAAAATGTCT TGCATTATAC AGCAACCTTT 1080

TGGGAATGAG TGGATGGATT GAATAAAATT TGATTAAGAG TGGATGATTT ATCTGTAGAT 1140

TATTATTGGA CAGTTAGTCT TGAAGTAGTC TAAGAATTAG GTTATAATCA GTAGAAGCCT 1200

TGCTAATAAT GAGGAGGTTA GTTTATGTAT AGTAGACTGA ATCTAAAATA GTACGAAACA 1260

ATTGCTAAAA CATTTATAGA AATTAATTTT ACTTTCCCAA TCGATTTGTT CTCATCTTAT 1320

TTCAATCCGC TATATATTAT GGTATCGAAT CTTCATCAGA ATGATAAAAT TAATCAATTG 1380

ATATCTGATT ACAAACAGAA TATGAAAGCT TTTTATATCA CTATTGAAAA ATTTATACGA 1440

GATGATGAAA GCCTTAAGTG TTATTTTATA AAGGTTATTT CAAGTCGTTC CAAGGTAACA 1500
AGTCTAGATC AGATTGAAGC TGATAAAACG ATACAAAGAA AATATTCAAG TGAGCTAAAA 1560
AAATTTATTG GATTTTATAA TGAGATTATT TGTGAGGAAA ATAGTTTCCT ACATGTACGA 1620
AAGAGGTGGT CGAGTTGGTT TAGGTAGTCG ATGCGTGAGT TGATAATTCT CAGGGTATGG 1680
ACTTCTTTTT CATGAATGAG GTAAAAGAGC AGGTATTGTT TAGAGACAAT CATTCTGAGC 1740
ATATTTTCTG GATAGAGGGA GTATCCGATT TTATGATCAA AGTTAATACC GCCCTCTGGT 1800
GAGAAGATGA GTAGGTTGGT AATTTAAACT ATTAAACAGA ATTTTTGATT AAAAGTATTA 1860
TTTCATGAGA GAAATCCTAA TTTCACAATC CATAGGCAAA CGCTTGCATT TCGTTTTTTA 1920
TTGGACTATA ATAGGTTGGT ATAAAGCCTT CTGTAGTAAT AAAATGTAGA AGGTGTAGAA 1980
AGTAAGGATT TAGAATATTT GTAGTTAAAA ACACAATGTT GCTATTCCTT ACGATAGGGA 2040
GATAGATATG GCAATGATAG AAGTGGAACA TCTTCAGAAA AATTTTGTGA AGACTGTTAA 2100
GGAACCGGGC TTGAAGGGGG CTTTGCGCTC CTTTATTCAT CCTGAAAAGC AGACCTTTGA 2160
AGCGGTCAAG GATTTGACCT TTGAGGTTCC AAAAGGGCAG ATTTTAGGAT TTATCGGGGC 2220
AAATGGTGCT GGGAAGTCGA CAACCATTAA AATGCTGACA GGAATTTTGA AACCAACATC 2280
TGGTTTTTGT CGGATTAACG GCAAGATTCC CCAGGACAAT CGGCAAGATT ATGTCAAAGA 2340
TATTGGCGTA GTCTTTGGAC AACGCACCCA GCTATGGTGG GATTTGGCTC TGCAAGAGAC 2400
CTACACTGTC TTAAAAGAGA TTTATGATGT GCCAGACTCG CTCTTTCATA AGCGTATGGA 2460
CTTTTTGAAT GAAGTCTTGG ATTTGAAGGA CTTTATCAAG GATCCCGTGC GGACTCTTTC 2520
ACTGGGACAA CGGATGCGGG CGGATATTGC GGCCTCCTTG CTCCACAATC CCAAGGTTCT 2580
TTTTTTAGAT GAGCCGACCA TTGGTTTGGA CGTTTCGGTT AAGGATAATA TTCGTCGGGC 2640
AATTACTCAG ATCAATCAAG AGGAAGAAAC TACCATTCTT TTGACCACTC ACGATTTGAG 2700
TGATATTGAG CAACTTTGTG ATCGGATTTT CATGATTGAC AAGGGGCAAG AGATTTTTGA 2760
TGGAACGGTG AGCCAACTCA AGGAGACCTT TGGTAAGATG AAGACTCTCT CTTTTGAACT 2820
GCTACCAGGT CAAAGTCATC TCGTCTCTCA CTATGACGGT CTGTCTGATA TGACCATTGA 2880
TAGACAAGGA AACAGCCTCA ACATTGAATT TGATAGTTCT CGCTACCAGT CAGCTGACAT 2940
TATCAAGCAA ACCCTGTCTG ATTTTGAAAT CCGCGATTTG AAGATGGTGG ATACGGATAT 3000
TGAGGATATT ATCCGTCGCT TCTACCGAAA GGAGCTCTAG GATGATCAAA TTGTGGAGAC 3060
GTTATAAACC CTTTATCAAT GCAGGGGTTC AGGAGTTGAT TACTTACCGA GTCAACTTTA 3120
TTCTCTATCG GATTGGCGAT GTCATGGGGG CTTTTGTGGC CTTTTATCTC TGGAAGGCTG 3180

TCTTTGATTC TTCGCAAGAG TCTTTGATTC AGGGCTTCAG TATGGCGGAT ATCACCCTCT 3240

ACATCATCAT GAGTTTTGTG ACCAATCTTC TGACTAGATC CGATTCGTCC TTTATGATTG 3300

GGGAGGAGGT CAAGGATGGC TCCATTATCA TGCGTTTGTT GCGACCAGTG CATTTTGCGG 3360

CCTCCTATCT TTTCACCGAG CTTGGTTCCA AGTGGTTGAT TTTTATCAGC GTTGGCCTTC 3420

CATTTTTAAG TGTCATTGTC TTGATGAAAA TCATATCGGG TCAAGGTATT GTAGAGGTGC 3480

TAGGATTAAC TGTCATTTAT CTTTTTAGCT TAACGCTCGC CTATCTGATT AACTTTTTCT 3540

TTAATATTTG CTTTGGATTT TCAGCCTTTG TGTTTAAAAA TCTTTGGGGT TCCAACCTAC 3600

TTAAGACTTC CATAGTGGCT TTTATGTCGG GGAGTTTGAT TCCCTTGGCA TTTTTTCCAA 3660

AGGTTGTTTC AGATATTCTC TCCTTTTTGC CTTTTTCATC CTTGATTTAT ACTCCAGTTA 3720

TGATCATTGT TGGAAAATAC GATGCCAGTC AGATTCTTCA GGCACTCCTT TTGCAGTTCT 3780

TCTGGCTCTT AGTGATGGTG GGATTGTCTC AGTTAATTTG GAAACGGGTC CAGTCCTTTA 3840

TCACCATTCA AGGAGGTTAG TATGAAAAAA TATCAACGAA TGCATCTGAT TTTTATCAGA 3900

CAATACATCA AACAAATCAT GGAATATAAG GTAGATTTTG TGGTTGGTGT CTTGGGAGTC 3960

TTTCTGACTC AAGGCTTGAA TCTCTTGTTT CTCAATGTCA TCTTTCAACA TATTCCATTC 4020

CTAGAAGGCT GGACCTTTCA AGAGATAGCT TTCATTTATG GATTTTCCTT GATTCCCAAG 4080

GGAATGGACC ATCTCTTTTT TGACAATCTC TGGGCACTAG GGCAACGCCT AGTCCGAAAA 4140

GGGGAGTTTG ACAAGTATCT GACTCGTCCC ATCAATCCTC TCTTTCACAT CCTAGTTGAA 4200

ACCTTTCAGA TTGATGCCTT GGGTGAACTC TTAGTCGGTG GTATTTTATT GGGAACAACA 4260

GTGACCAGCA TTGTTTGGAC TCTTCCAAAA TTCCTGCTTT TCCTAGTTTG TATTCCTTTT 4320

GCGACCTTGA TTTATACTTC TCTTAAAATC GCAACAGCCA GTATCGCCTT TTGGACTAAG 4380

CAGTCAGGCG CCATGATTTA CATCTTCTAT ATGTTCAATG ACTTTGCTAA GTATCCGATT 4440

TCTATTTACA ATTCTCTTCT TCGTTGGTTG ATTAGCTTTA TCGTGCCTTT CGCCTTTACA 4500

GCCTACTATC CAGCTAGCTA TTTCTTACAG GAAAAGGATG TGTTCTTTAA CGTAGGAGGT 4560

TTGATGTTGA TTTCTCTGGT TTTCTTTGTT ATTTCCCTTA AACTTTGGGA TAAGGGCTTA 4620

GATTCCTACG AAAGTGCGGG TTCGTAAAAG CTAAAGTAAG ACTAAAATCA AGAAAGAAAC 4680

TTATGATGTT TGTAATTGAA GAAGTCAAGG ATGAAAATCA AAAAAAGGCA GTTGTCGCTG 4740

AGGTTTTGAA GGATTTGCCA GAATGGTTTG GAATCCCAGA AAGCACACAA GCCTATATAG 4800

AAGGAACCAC GACACTGCAA GTTTGGACCG CCTATCAGGA GAGTGATTTG ACTAGATTTG 4860

TAAGCTTATC CTATTCGAGT GAAGATTGTG CAGAGATTGA TTGTCTCGGC GTAAAAAAGC 4920

TTATCAAGGT AGAAAAATTG GGAGCCAATT GCTTGCTACT TTAGAGAGTG AAGCTCGTAA 4980

AAAAGTTGGT TATCTGCAGG TCAAAACAGT GGCAGAAGGT TCTAATAAAG ATTATGATCG 5040

AACAAATGAC TTTTATCGAG GTCTTGGCTT TAAAAAGTTA GAGATTTTTC CTCAACTATG 5100

GAATCCGCAA AATCCTTGTC AGATTTTGAT TAAAAAGCTT GAATAATATT ACTTGACATC 5160

TATTCTCAGA GTGCTATACT GTAAGTGTAA TCGCCGATTT AGCTTAGTTG GTAGAGCAAG 5220

GCACTCGTAA AGCCTAGGTT ATAGGTAGAT AAACGACTGA GGATTTGAAA AAATAGATAG 5280

GTAGAAGATA ACCGTTAAGC CTTACTCTTA GCGGTTATTT ATATTGTTTA ATAGCGCTAA 5340

TATTTTATCA ATTATGCCTG TTTTCGTGTT TCTGGTAGTT GTTCAAGTTT ATTGCTACTA 5400

TTTTTGATGG TATGAATGTG CTTATAATGT ATCCCGGTTA ACGAAAGTTT TGGACTTATA 5460

CTCTTCGAAA ATCTCTTCAA ACCACGTCAA CGTCGCCTTG CCGTGCGTAT GGTTATGACT 5520

TCGTCAGTTC TATCCACAAC CTCAAAACAG TGTTTTGAGT GACTACGTCA GTTCCATCTA 5580

CAACCTCAAA ACACTGTTTT GCCCAATCTG CGGCTAGTTT CCTAG 5625

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CTCTCCAGCT TTCCTTGCGA GTTGGCCATG TTGTGTCTTT AAGAAGTCTA AAAATATCTC 60

CAATAAAACG CATCGCTCTC TCCTATCTCG TTTCTCTGTG TGTAGTGTAC TTGCCACAAT 120

GCTTACAAAA TTTATTTACT TCTAGTCGTG TAGGCTTGAG GTTTCCGCTG ATCTTGATTG 180

AATAGTTTCT CGAACCACAA ACCGCACAAG CTAGGCTTGC TTTTTTTAGT GCCATAACGC 240

CTCCATCTTA TCCATTATAA CAAGAAAGCT AGGCTTTGAC AAGCATCTTA GCGAAATAGA 300

TTGACTATCG AATCCCATAT TGTTTGAGCC TTTTCCTTAA TCTTCGCATC TGAGATAGCC 360

CGGCTAGCCT CATCTACTAG ACTTTGCGCA CGCCCTCGAA TATCAGACAA ATTATCATCT 420

GTCTGGCTAT TATCATTGGT TTGTACTTGT CTTTTTGTAT TGGCTGGTGC AATTCCATTT 480

TGCTTATAAG CATTTTCAAC CGTAAAGGTA CTTCCTGGCG TATAAGGTAA AATGGTATTG 540

GCAATGTTTC TAAAGACATG AGCTGCACCG TTTGAAGTAG AGCCAGCTAG ATAGTGGTTT 600

TCATCAGTGG TCGGAAAGCC AAGCCAGTGG CTAATCACTA CATCCGGAGT ATAACCAATT 660

ACCCACTGGT CACTTGTGTA CTCCGGATTG AAAACTGCTT CAGTTGTTCC AGTTTTCCCT 720

GCCATGACAT AGTCTGCAGG CGATGAACTA ATACCGGTAC CGTTGGTGAA AGTCCCCAAC 780

ATCATACTGG TCATCTTGTC AGCTACAGAC TTATCAATCA CCCGTTTTTG TGAATTTTTA 840

TGACTCGCAA TAACTTGTCC ACTAGCATTT TCAATTCTAC TAATAAAATG AGCTTCAGGC 900

ATTAAACCTT CATTTGCAAA GGCGGCGTAT GCTTGAGCCA TTTGAAGAGG GTTGGTTTCA 960

ACACCGCTTC CCAAGGCGAC ACCAAGAACA CGGTCGACCT TTTCCATGTT GAGTCCGAAT 1020

TTTTCGCCTG CCTCAAAAGC CTTGTCGACA CCCAAATCAT TAACAGTGGC AACAGCAGGT 1080

AGATTAAGCG ATTCTGCCAA GGCTTGATAC ATAGGAACTT CTCGACTCGT TTTGATCCCT 1140

GCATAGTTAT CAACCTTATA GCTGTCATAC TGCATGGTAT GGTTATCCAA CTGCTTATTC 1200

AAAGCCCAGC TTGCTTCAAC TGCTGGCGTA TAAACAACTA AAGGCTTAAT TGTAGAACCA 1260

GGACTACGCT TTGATTGGGT TGCATAGTTG AAATTCCGGA ATCCAGTTTT ATCATTGTCA 1320

GCAACTTGAC CGACAACTCC ACGAACTCCC CCTGTTTTCG GTTCGAGGGC TACACTTCCT 1380

GATTGAGCAA ACGTTCCATC CTCTGCCCTC GGAAATAGCG ATGTGTTTTC ATAAACAATC 1440

TGCATATTTG CTTGGTAGTT TTGGTCCAGC TCTGTGTAAA TGCGGTAGCC ATTATTGACA 1500

ATCTCTTCCT CTGTTAGATT ATACTTGGAA ACAGCTTCAT TAACCACCGC ATCAAAATAA 1560

GAGGGGTAAC GGTAATCTGA GATTTTTCCT TCATACTTAT CGTGCAATTG CGAAGTCATA 1620

TCAACTTCAG CAGCTTTGGT TTCTTGGTTT TTATCAATAT ATCCTGCTGC AACCATATTC 1680

TGCAAGACAG TATCGCGCCG ATTAGTAGAA TCTTCTACGG AATTCAAGGG ATTATACAGT 1740

TCCGGCCCCT TGAGCATCCC TGCCAGAGTC GCAGCTTGAT CCAGACTCAC TTCTGATGCA 1800

GAAACTCCAA AGTATTTCTT ACTCGCATCT TCTACACCCC ACACACCATT TCCAAAATAA 1860

GCGTTGTTAA GGTACATGGT TAGAATTTGC TCCTTACTAT ATTTTTTGCT TAATTCTAAG 1920

GCAAGGAAAA ATTCTTTCGC TTTTCTCTCA ACAGTTTGAT CCTGCGATAA ATAGGCGTTT 1980

TTAGCCAGCT GTTGGGTAAT GGTAGAGCCA CCACCTGAAC GTCCAGCAGT GACAATAGCC 2040

AAGAAAAAAC GGCCATAGTT AATCCCGTCA TTTTTATAGA AAGAACGGTC TTCTGTCGCA 2100

ATAACAGCAT TCTGCAAGTT TTTACTGATG TCAGTCAGCT CAACATAGGT TCCCTTTTGA 2160

CCAGACAAGG CACCAGCCTC TTTTTCTTCA CGGTCAAAAA TAAGAGTCCG AGTTTTCAAG 2220

GCATTTTGCA AATCATTGAC ATTGGTCGAC TTGGCTACAG CAAACAAATA GATTCCAACT 2280

AGCAAGCCTG CACTCAAACC TAGTATAAGG ATAATCTTTG TTAGATGATA ACGACGCCAG 2340

AATTTTCGAA TCGGACCTAC TTGGGCTAAT TTTTTTCGAT CACTACGAGA GCGACGTAAG 2400

ATAGTAGAAT CAGAGTCCTC TAGTTCACTT GTTTCTTTTT TAAAAAGAGA AAGAAATTTC 2460

TCAAATAATT TATCTAATTT CATGCGTTTA TTTTATCATC TTCATCATAG GAAGACAAGA 2520

ATTTAGCTAT TTCCTATCCA AATAGGGCTT TTTTTGTTAC AATATCTGTA TGCAATTCAC 2580
ATTTACATTA CCCGCCTCTC TACCTCAAAT GACAGTAAAG CAATTACTTG AGGAACAACT 2640
CCTCATCCCT AGAAAAATCC GTCATTTTTT GAGAATCAAG AAACATATTT TGATAAATCA 2700
AGAAGAAGTC CACTGGAAGG AAATCGTAAA TCCTGGAGAT GTTTGCCAGT TGACTTTTGA 2760
CGAGGAAGAT TATTCCCAAA AGACGATCCC TTGGGGCAAC CCAGACTTAG TGCAGGAAGT 2820
TTATCAAGAT CAACACTTGA TTATTGTAAA CAAACCAGAG GGGATGAAAA CGCATGGTAA 2880
TCAACCAAAC GAAATTGCCC TTCTTAACCA TGTCAGTACC TATGTTGGCC AAACCTGCTA 2940
TGTCGTTCAT CGTCTGGACA TGGAAACCAG TGGCTTAGTT CTCTTTGCCA AAAATCCTTT 3000
TATCCTGCCC ATTCTCAATC GCTTATTGGA GAAAAAAGAG ATTTCTAGAG AATATTGGGC 3060
TCTAGTTGAT GGAAATATCA ACAGAAAAGA ACTTGTTTTC AGAGACAAAA TTGGACGTGA 3120
TCGCCATGAT CGTAGAAAAA GAATAGTTGA TGCAAAAAAT GGGCAATATG CTGAAACGCA 3180
TGTAAGCAGA TTAAAGCAAT TCTCAAACAA GACTTCCTTG GCTCATTGCA AGCTAAAGAC 3240
AGGGCGAACC CATCAGATTC GTGTGCACCT TTCGCATCAT AATCTTCCTA TCCTGGGAGA 3300
CCCTCTCTAT AATAGTAAAT CAAAGACAAG CCGGCTTATG CTTCATGCCT TCCGACTTTC 3360
CTTTACCCAC CCACTTACTT TAGAGAAGCT AACTTTCACT ACCCTTTCAA ATACATTTGA 3420
AAAAGAATTA AAAAAGAATG GATGATCGTG TCATCCATTT TTCCATATAA AAAAGCAAGA 3480
CCACAAAGCC TTGCTTTCTA TCAACTCAAG AATTATTTAG CAATTTTTGC GAAGTATTCA 3540
AGAGTACGAA CAAGTTGTGC AGTGTATGAC ATTTCGTTGT CGTACCATGA TACAACTTTA 3600
ACCAATTGTT TACCGTCAAC GTCAAGAACT TTAGTTTGAG TTGCGTCAAA CAATGAACCG 3660
TAAGACATAC CTACGATATC TGAAGATACG ATTGGATCTT CTGTGTAACC GTATGATTCG 3720
TTTGAAGCTG CTTTCATAGC TGCGTTCACT TCATCAACAG TAACGTTCTT TTCAAGAACT 3780
GCTACCAATT CAGTAACTGA TCCAGTTGGA GTTGGAACGC GTTGTGCAGA TCCGTCAAGT 3840
TTACCATTCA ATTCTGGGAT TACAAGACCG ATAGCTTTTG CAGCACCAGT TGAGTTAGGA 3900
ACGATGTTTG CAGCACCAGC GCGAGCACGG CGAAGGTCAC CACCACGGTG TGGTCCGTCA 3960
AGGATCATTT GGTCACCAGT GTAAGCGTGG ATAGTAGTCA TCAATCCTTC AACAACACCA 4020
AAGTTGTCTT GAAGAGCTTT AGCCATTGGA GCCAAGCAGT TTGTAGTACA TGAAGCACCT 4080
GAGATAACTG TTTCAGTACC GTCAAGAACG TCGTGGTTAG TGTTGAATAC AACTGTTTTA 4140
ACGTCGTTTC CACCAGGAGC AGTGATAACA ACTTTTTTAG CTCCACCTTT AAGGTGTTTT 4200
TCAGCTGCTT CTTTCTTAGC AAAGAAACCA GTAGCTTCAA GAACGATTTC TACACCGTCA 4260

GTAGCCCAGT CGATTTGTTC TGGATCACGT TCAGCAGAAA CTTTGATGAA TTTACCGTTA 4320

ACTTCAAATC CACCTTCTTT AACTTCAACA GTACCGTCGA AACGACCTTG AGTTGTGTCG 4380

TATTTCAACA AGTGTGCAAG CATAACTGGA TCTGTAAGGT CGTTGATGCG TGTAACTTCA 4440

ACACCTTCTA CGTTTTGGAT ACGACGGAAA GCAAGACGAC CGATACGTCC GAAACCGTTA 4500

ATACCAACTT TAACTACCAT TAGTGATTTC CTCCTTATGA AAATCATGAA ATTTTTATTG 4560

TGAAAAGAGT AACTTGAATC ACTACAAATC ACCTTTCAAC AAACCTATTA TACAACTATT 4620

TGAGTTGAAT TGCAAGTATG GCCATTGTTT TTCTATGTTA GTTTCTTTTT AAGACTGTAA 4680

ACCAAGGAAT CCCTTACTAT TCATAGCATA ACGATTCTAT AGGATCCATT TTACTAATCT 4740

TACGCGCCGG GAAGTAGGCT GAGACATAAC CAAGTAATAG AGCGAAAACT AGAGTTCCTA 4800

AAACAGATAA AAGATTTAAT TTAAAAACCT TAGTGATGGA TGGGTAAAAG TGACTTACAA 4860

TCGCATTCGC CAAACTTCCC ACCCCTTGTG CAACCAAAAA TGCCAGCAGC AAGGCGATGC 4920

CTACAATCCA GATAGCCTCG TAAATAAAAA TTCCTTTGAC ATCACGATTC TGATAACCAA 4980

CTGCTTTCAT GACACCTATT TCCTTGGAAC GTTGCATGAT ATTGATGTAA ATAATGATAC 5040

CAATCATAAC CGCTGCTACC ACAATAGCTT GTGATGAAAG CACAATCAAT AATCCCTGAA 5100

TAACACGAAT AAAGGTAATC ACAATATCAA GAACTCTCTG TTGAGAAAGC ACAGTATACT 5160

TCTTATTTTT CTGTAATTCT TCTGTTACTA CTTTTGTCTG TGATGGATCT TTGAGTTCCA 5220

AGATAAAATA AGATACAGCT TTCGTAAATC CAGCCTCTTT CAAAATCGTT TCCATTTGAT 5280

GAGACAGCAT GAAACTGTTG CTGTCCTCCA TGTCATCTTC ATCATTGATT ACACGTACAA 5340

TCTTCGTTTG AAATTGAGCA ATCTTACTAG TTTCGGCAGC ACTTTCTACA ATGCTGGCTG 5400

AGACTGATTT GCCAATAAGA TCATTAGCTG TCAAATTTTT TCCTGTCTGT TCATTCCAAT 5460

TTTTTAGTAA ACTGCTTGGA ATCGTTAATC CCTGTTCATT TGTATCAGTA TAGAGGGATC 5520

CAGCCAACAC TTTGTCCGTC TCATTATTAC TAACAGAGAT ACTTGTATCA TCATAAAGAC 5580

TCACTACTTG AGCATAAGAA GGCATCGTTT GACTCAGATC CATTTCTTGC CCATCTATAG 5640

TAATATTTGA CATGTTCATC CCAAAAGGAC TCTCCAAATA TTTAATAGCT TCTTTCCCAA 5700

CTGTATCCGT GATATATAGT CAATTGAAAC AAGAGCAGGA TAAAAAAGCC TCGTAAAAGG 5760

TATTGCAACT TGGTAATACC TTTTTGAGGT GCTTTTTGAT ATGAGCCCAT GTTTTCTCAA 5820

TAGGATTGTA CTCAGGCGAG TAGGGAGGAA GAGGTAAAAG TTTATGCCCA AACTCTTCGC 5880

ATAAAAGTTC TAGCTTCCCC ATTCTATGGA ATCTTACATT ATCCATAATA ATAACCGATG 5940

GTGTGTTTAA TGTTGGTAAG AGAAAATTCT GAAACCAAGC TTCAAAAAAG TCGCTCGTCA 6000

TCGTCTCTTC GTAAGTCATT GGAGCGATTA ATTCACCATT TGTTAGACCT GCAACCAAAG 6060

AAATCCTCTG ATATCTTCTT CCAGATACTT TGCCTCTTAT TAATTGACCT TTTAATGAGC 6120

GACCATATTC TCGATAAAAA TAAGTATCGA ATCCTGTTTC GTCAATCTAA ACAGGTGCTA 6180

GGTGCTTTAA ACTATTAAAA TTCTTAAGAA ATAAGGCTAC TTTTTCTGGG TCTTGTTCAT 6240

AGTAGGTGTG GTTCTTTTTT CGAGTGTAGC CCATAGCTTT GAGCGTATAG TGGATGGTAG 6300

TTGGATGACA GCCAAATTCA GAAGCTATTT CAGTCAAATA AGCGTCTGGA TTGTCAGTAA 6360

GATAGTTTTT AAGTCTATCT CTATCAACCT TTCTTGGTTT TATTCCTTTT ACTTGGTGGT 6420

TTAGCTCTCC TGTTTTCTCT TTTAGCTTTA ACCAGCCATA AATGGTATTA CGTGAGATTT 6480

GGAAAACGTG TGATGCTTCT GTTATACTAC CTGTTCGCTC ACAATAAGAG AGAACTTTTT 6540

TACGAAAATC TATTGAATAT GCCATAAAAA GATTATACCA CATTGTGTAC TATTTTTGGT 6600

TCATTTTACT ATATTTGAAG AGGCGTTTAA ACTATCTGAC ATAAAACTCG TTCTAGAGGA 6660

AAGACATCCT TTAAAAAGTT AGTTTATTTT ACAACTTAGA CATCAAGGTA GGTTAACCCC 6720

TTCATGGAAA AATCAAGACT CTTAGCACTA TGGGTTAAAC TACCACTGGA GACGTAATCA 6780

ATCGCTAAAC CACGAAAACG GCTAATAGTG GTCATATCAA TATTTCCAGA ACATTCAATC 6840

CGAGAACGTC CTGCAATTAG GGTAATGGCC TGTTCAATCT GTTCCAATGA CATATTATCC 6900

AACATGATAA TATCAGCACC CGCCGCCGCA GCTTCTTCGG CAGCAGCAAG GCTTTCCACT 6960

TCCACCTCGA CCATTTTCAC AAAAGGGGCA TAGGCACGCG CTTGAGCAAT TGCCTTTTGA 7020

ACACTACCTA CTGCCGCAAT GTGATTGTCT TTTAGCAGGA TAGCATCTGA TAAATTAAAG 7080

CGATGATTAT AGCCACCGCC AACTCTCACG GCATATTTCT CAAAAAGACG TAAATTAGGA 7140

GTAGTTTTTC GAGTATCAAA TACCTTAATG CAATCATCGC CTAAGGCTTC TACATAAGCA 7200

GCTGTCATCG AAGCAATCCC TGATAAATGT TGTAAAAAAT TCAAGGCAAC GCGTTCACAT 7260

GTTAAGAGAC TTCTCACCGA GCCTATGATT TCTAAAACCA AATCGCCACT AGTCAAACGA 7320

TCCCCATCCT TAAATTGATG AGGATTCTGG AAGGTCACCT CGGCATCAAA TAGGGTAAAA 7380

ACCCTTTGAA AAACGGTTAG CCCCGCTAAA ACACCAGCTT CCTTGGCAAA AAGCGACACC 7440

TTGGCTTGGC CATGATGATC AAAAATGGCA TTGGTACTGT AATCTTCGGA ATGAACATCT 7500

TCTCGCAAGG CTGCTTTCAA TGTATCATCT ATTTGAAAAG GGGTTAAATC AGTTGAAATG 7560

ATTGACATCA C 7571

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTTGCTAGTG GCTTAAATTC TTCAGGAAAA TCAGGCGTAT CTAAAAGTCG TGTCGTTTTT 60
GTTTCATCTA TATAAAGACT TCCTGCTCCC CCTACAACTA GAAAACGTGT CTGTGTTCCA 120
GCAAGAAGCT GATTAAATAG TTCGATTGAT TTGCTGTGGA GCGGTAGCGT ATCTGGTGTA 180
TAAGCACCAA ACGCTGAAAT AACAGCATCA AATCCAGTAA GATCATCTTT TGTCAACTCA 240
AATAAATCTT TTTTAATAAT AGACTCAGCT TGACTTTTGT TTTCAGAACG AACAATAGCC 300
GTTACTTCAT GTCCTCGTTT GACTGCTTCT TCAACAATTG CTTTCCCCGC TTGTCCATTT 360
GCTGCAATAA CTGCTAGTTT CATTTTTTAT ACCTCTCTTG TTGTAATTAT TTTAGTTACA 420
GAAATTGTGA CACTCTTAAT AATCAATGTC AATAGTCTTG CTTAATTATT ATCAAAATAT 480
TTCTACCAAG AAAACTAACC ATGATTCTAG TGAAAAAAAA TCTTCTTTGT CAACAAATTT 540
ACTTTCTTGT TTTAAACATG CTATAATAAT CATAGCAAGA GATCTAAGTT GTCTGTTTTT 600
TTAAAACGAG GTGATTATCA TGCGTAGATT CTATTCCCAT CTCCCCTACT ATCTGGTCAT 660
ATTATTCTTT TATTGGCCAC TTTATGAGTT GTTCTTACTA GTTGTTTCTG ACCCCCTTAC 720
ACTCAAGGGA CTCTATATAA ACAATCTTCT CTTCTTTACA CCTCTGGTAA TCTTGATTGT 780
ATCGTTACTC TATAGCTACC GTTTCCGTTT CTCACTTTGA TGGTTAGTTG GTAACGGACT 840
GCTCTTTTAC TTTACTATCA TAACCTTTGG TGAGTTTATA CTAATTTACT TGCTAATCTA 900
TGAAACAGTT GCTCTGGTCG GCATGGATTC TGGTATTAGC ATCAAGCATA TTCTACAAAA 960
AATGAAAAAC AAAAAACTTT CACAAAATCC TTGAAAAATC TCACAATCAT GCTATAATAA 1020
TCCATAGAGA CAAGTCACTT AGTCCCTTTC TACTAGAGAG TGCGTGGTTG CTGGAAACGC 1080
ATAGGAAGTC TAAACTGATA CTACTCTTGA GTTTTTTATG AAAACATAAA ACGGTGGCCA 1140
CGTTAGAGCC GATCAGAGGT GTCCCTCTCT TTTGAGGTAC ATAAATGAAG GTGGAACCAC 1200
GTTGCGACGT CCTTTCGAGG ATGTCGCATT TTTTTATTAG GATACTAATT ATGGAGTTGC 1260
AAGAATTAGT GGAGCGCAGT TGGGCAATCC GACAAGCTTA TCACGAACTG GAAGTTAAGC 1320
ATCATGATTC CAAGTGGACG GTAGAAGAAG ACCTCTTGGC TTTATCTAAT GATATTGGAA 1380
ATTTCCAACG ACTGGTGATG ACAAAGCAAG GACGCTACTA TGATGAAACA CCCTACACAC 1440
TGGAACAAAA ACTTTCAGAA AATATCTGGT GGCTATTAGA ACTTTCTCAA CGTTTGGATA 1500
TAGACATTCT GACGGAAATG GAAAACTTCC TCTCTGATAA AGAAAAGCAA TTGAACGTTA 1560
GGACTTGGAA GTAGTCTGCT GATAAAAAAT CAATGCTTAG AAACTATGAA ATAATAAAAA 1620

AGGAGAACAT CATGATTAAC ATTACTTTCC CAGATGGCGC TGTTCGTGAA TTCGAATCTG 1680
GCGTAACAAC TTTTGAAATT GCCCAATCTA TCAGCAATTC CCTAGCTAAA AAAGCCTTGG 1740
CTGGTAAATT CAACGGCAAA CTCATCGACA CTACTCGCGC TATCACTGAA GATGGAAGCA 1800
TCGAAATTGT GACACCTGAT CACGAAGATG CCCTTCCAAT CTTGCGTCAC TCAGCAGCTC 1860
ACTTGTTCGC CCAAGCAGCT CGTCGTCTTT TCCCAGACAT TCACTTGGGA GTTGGTCCAG 1920
CCATCGAAGA TGGTTTCTAC TACGATACTG ACAACACAGC TGGTCAAATC TCTAACGAAG 1980
ACCTTCCTCG TATCGAAGAA GAAATGCAAA AAATCGTCAA AGAAAACTTC CCATCTATTC 2040
GTGAAGAAGT GACTAAAGAC GAGGCACGTG AAATCTTCAA AAATGACCCT TACAAGTTGG 2100
AATTGATTGA AGAACACTCA GAAGACGAAG GCGGTTTGAC TATCTATCGT CAGGGTGAAT 2160
ATGTAGACCT CTGCCGTGGA CCTCACGTTC CATCAACAGG TCGTATCCAA ATCTTCCACC 2220
TTCTCCATGT AGCTGGTGCG TACTGGCGTG GAAACAGCGA CAACGCTATG ATGCAACGTA 2280
TCTACGGTAC AGCTTGGTTT GACAAGAAAG ACTTGAAAAA CTACCTTCAA ATGCGTGAAG 2340
AAGCTAAGGA ACGTGACCAC CGTAAACTTG GTAAAGAGCT TGACCTCTTT ATGATTTCAC 2400
AAGAAGTGGG ACAAGGTTTG CCATTCTGGT TGCCAAATGG TGCGACTATC CGTCGTGAAT 2460
TGGAACGCTA CATCGTAAAC AAAGAGTTGG TTTCTGGCTA CCAACACGTC TACACTCCAC 2520
CACTTGCTTC TGTTGAGCTT TACAAGACTT CTGGTCACTG GGATCATTAC CAAGAAGACA 2580
TGTTCCCAAC CATGGACATG GGTGACGGGG AAGAATTTGT CCTTCGTCCA ATGAACTGTC 2640
CGCACCACAT CCAAGTTTTC AAACACCATG TTCACTCTTA CCGTGAATTG CCAATCCGTA 2700
TCGCTGAAAT CGGTATGATG CACCGTTACG AAAAATCTGG TGCCCTCACT GGCCTTCAAC 2760
GTGTACGTGA AATGTCACTC AACGACGGTC ACCTATTCGT TACTCCAGAA CAAATCCAAG 2820
AAGAATTCCA ACGTGCCCTT CAGTTGATTA TCGATGTTTA TGAAGACTTC AACTTGACTG 2880
ACTACCGCTT CCGCCTCTCT CTTCGTGACC CTCAAGATAC TCATAAGTAC TTTGATAACG 2940
ATGAGATGTG GGAAAATGCC CAAACCATGC TTCGTGCAGC TCTTGATGAA ATGGGCGTGG 3000
ACTACTTTGA AGCCGAAGGT GAAGCAGCCT TCTACGGACC AAAATTGGAT ATCCAGATTA 3060
AAACTGCCCT TGGAAAAGAA GAAACCCTTT CTACTATCCA ACTTGATTTC TTGTTGCCAG 3120
AACGCTTCGA CCTCAAATAC ATCGGAGCTG ATGGCGAAGA TCACCGTCCA GTCATGATCC 3180
ACCGTGGGGT TATCTCAACT ATGGAACGCT TCACAGCTAT CTTGATTGAG AACTACAAGG 3240
GGGCCTTCCC AACATGGCTG GCACCACACC AAGTAACCCT CATCCCAGTA TCTAACGAAA 3300
AACACGTGGA CTACGCTTGG GAAGTGGCCA AGAAACTCCG TGACCGCGGT GTCCGTGCAG 3360

ACGTAGATGA GCGCAATGAA AAAATGCAGT TCAAGATCCG TGCTTCACAA ACCAGCAAGA 3420
TTCCTTACCA ATTAATTGTT GGAGACAAAG AAATGGAAGA CGAAACAGTC AACGTTCGTC 3480
GCTACGGCCA AAAAGAAACA CAAACTGTCT CAGTTGATAA TTTTGTTCAA GCTATCCTAG 3540
CTGATATCGC CAACAAATCA CGCGTTGAGA AATAAGAGTC TAGCATAAAA GCCTCCAATC 3600
TGGAGGCTTT TTCTCATCTA TTTTTACTCA AGGACTAAGT TCACTTGAGC AAACTGAATC 3660
CGCACTGTCG TTCCTTTTCC GACCTCAGAC TCGATACGAA TCTGGTGCCC CAGTTCTTCA 3720
GAAATTTTCT TAGATAGATA AAGGCCAAGT CCAGAGGACT GCTGGGTCAA ACGGCCATTG 3780
TATCCTGAAA AGCCACGTTC AAATACTCGG AGGACATCAC TGTTTTTTAT CCCGATTCCC 3840
GTATCTTTGA TACAAAGCTC TTGGTCATCC ATATAAATCT CCAGACCACC TTCCTTGGTG 3900
TACTTGAGAC TGTTTGAGAT GATTTGCTCA ATAACCACTA GCAGCCACTT TTTATCCGTC 3960
ACGATTTCTT TATCAAGGTC ATGTAGATTG ACATTTAAGC CTTTTTGAAT AAAGAAAAGA 4020
GCATATTTAC GAATTATTTC CTTGACCAAG TCCTCAATTT GAACCTGCTT TAAGACCAAA 4080
TCATCATGGA AACTTTCTAA ACGCAGGTAC TGTAAAACTA GGTTGGTATA GGAGTCGATT 4140
TTGAAAATTT CCTGTTCTAG CTGCTGCTTC AGTTGGCGGT CGACCACTTC TGCAACTAAG 4200
AGTTGACTGG CTGCAATGGG GGTCTTTATC TGATGGACCC ACAAGGTATA GTAATCCAGC 4260
AAATCCGTCA GTTTTCTTTC TGCTTTTGAC CTCTGCTGAT AGAGTTCCAT CTCACGCGCT 4320
TCTAATTTTT CTGCTAAAGC TATTTCCAAA GGAGACTTGG CTTCCCTCTC TCCATAGAGA 4380
AGTTCCTGGC GATAGACCTG CGTTTCCACC AATATGTCCC AAGTGAAAAA TAATATGGTT 4440
ACAAAGCAAC ACAAGAAGAA AAAGTAGAGG AAGTAAATTC CTAGACTGGC AAATAAAAAC 4500
TGAAAGAGTA AGACAAGAAA TGCCAAAGAA AGCAGATAGA TAAAAAGACG ACTACGGGAG 4560
CGCAGATAGG CTAGAAAAAA TTGTTTCCAA TCAAGCATGC TTCAATCCGT ACCCTATTCC 4620
TTTCTTGGTC TCGATAAATC CTACCAATCC CTGCTCCTCC AACTTTTTAC GCAAACGAGC 4680
CACATTGACA GAGAGGGTAT TATCATCAAT GAAAAAGTCA CTGTTCCAAA GTTCCCGCAT 4740
CAGGTCGTCA CGTGCTACGA TGTTGCCTGC ATGCTCAAAT AACACGCGTA AAATCTGGAA 4800
TTCATTCTTG GTCAAATTCA AGACTTGCCC TTGATAATGT AAATCCATGG ATTTGGTATT 4860
GAGGATAACA CCAGCATATT CCAGCAAACT CTCATCACGC CCAAACTCAT AGGAACGACG 4920
CAACAAGCCC TGAACCTTAG CTAAAAGAAC CTGCTGGTCA AAAGGCTTGG TCACAAAGTC 4980
ATCCGCCCCC ATATTGATTG CCATGACAAT ATCCATAGCC TGGTCTCTCG AAGAAAGAAA 5040
CATGATAGGT ACCTTGGAAA TCTTGCGGAT TTCCTGACAC CAGTGATAAC CATTAAACAA 5100
GGGCAAACCA ATATCCATGA GGACCAGATG AGGTTCCGAC TGAACAAATA GACTCAAAAC 5160

TTCCATAAAG TCTTCTACCA GGACCACTTC AAATCCCCAT TCAGAGAGCA TTTTCCCAAT 5220
CTGTTGACGA ATGACCTGAT CATCTTCTAT TAATAAAATC TTGTGCATGC GCTTCTCCTT 5280
TTCCATTATT ATAACAGATT TTTCCATGCT AGATGGTCTG AAACTGAATT TGAAATAGCC 5340
TGTTTTTAGC CAGTACAAAC AGGCTATGCT ACTAGCTAAT TTGAGGGAAA TTTGCTAAGA 5400
TAAATAAAAA GAAAGGAGCT CTTATGGCCA ATATTTTTGA CTATCTGAAA GATGTCGCAT 5460
ATGATTCTTA TTACGACCTT CCCTTGAATG AGTTAGACAT TCTAACCTTA ATAGAAATCA 5520
CCTACCTCTC CTTTGATAAT CTGGTCTCCA CACTTCCTCA ACGTCTTTTA GATCTAGCAC 5580
CTCAGGTTCC AAGAGATCCC ACCATGCTTA CTAGCAAAAA TCGCCTTCAA TTATTAGATG 5640
AATTGGCTCA ACACAAGCGC TTCAAAAATT GCAAACTCTC CCATTTTATC AACGACATCG 5700
ACCCTGAACT GCAAAAGCAA TTTGCGGCTA TGACTTATCG TGTCAGCCTC GATACCTATC 5760
TGATTGTCTT TCGTGGGACA GATGACAGTA TCATTGGCTG GAAGGAAGAT TTCCACCTGA 5820
CCTATATGAA GGAAATTCCT GCTCAAAAGC ACGCCCTTCG CTATTTAAAG AACTTTTTTG 5880
CCCATCATCC TAAGCAAAAG GTTATTCTAG CTGGGCATTC CAAGGGAGGA AATCTCGCTA 5940
TCTATGCTGC TAGCCAAATT GAGCAAAGTT TGCAAAATCA GATCACAGCA GTTTATACAT 6000
TTGATGCACC TGGTCTCCAT CAAGAATTGA CACAGACTGC GGGTTATCAA AGGATAATGG 6060
ATAGAAGCAA GATATTCATT CCACAAGGTT CCATTATCGG TATGATGCTG GAAATTCCTG 6120
CTCACCAAAT CATCGTTCAG AGTACTGCCC TGGGTGGCAT CGCCCAGCAC GATACCTTTA 6180
GTTGGCAGAT TGAGGACAAG CACTTCGTCC AACTGGATAA GACCAACAGT GATAGCCAGC 6240
AAGTAGACAC AACCTTTAAA GAATGGGTGG CCACAGTCCC TGACGAAGAA CTTCAGCTCT 6300
ACTTCGACCT CTTCTTTGGC ACTATTCTTG ATGCTGGTAT TAGCTCTATC AATGACTTGG 6360
CTTCCTTAAA GGCGCTTGAA TACATTCATC ATCTCTTTGT CCAAGCTCAA TCCCTCACTC 6420
CAGAAGAAAG AGAAACCTTG GGTCGCCTTA CCCAGTTATT GATTGATACT CGTTACCAGG 6480
CATGGAAAAA TAGATAATAC TCTTGAAAAT TAAATGTATA CAAAACAAAA GACCTAGAAT 6540
ACATACTTTC ATGTGCATTC TAAGTCTTTT TAAATAGAAT CTAATAGTCA ATAAAAATCA 6600
AAGAGCATTG AGAGATAATG GGGCTTGGAA CGTCCCTCTC GCTTCAACAA AATGACCCCA 6660
TTATAGATTA AAAAGATGCC ACTTAGAAAA AGCAAAAAAG GAAGTAAGAC AAAGGCAAAT 6720
ATATAAAAAG CTAACTGAAC ATTCTCGTAT CCATTTTTAT AAAAAAGGTA GGATAGATAA 6780
AAATAACTTG AAATGAGGGA TAATAAAAAT AATACTGGAT TCCACAAACT TCTATTATCC 6840
TTCCAAAATG ACACTATAAA GGCTAATACA ATTCCTATAA CGAGATACAT TTCTTACTCC 6900

TTTAATAGCT ACATTTTATC ATAATTATCC AAAGAAAAAA GAGGGCATTT ATCCCTCTTA 6960

ATCCTTCATC TGACTCTCTG CATCGGCCAC GACTTTTTCT AGACTGGTTT GACCAAGTTC 7020

TGCCTCCATA GTCAACTGAA TTCTCTCCAA TTTTTGATCC AAAACATCAT GAATATGAGC 7080

TCCTACAGGG CAATTTGGAT TCGGATTGTC ATGGAAACTG AAGAGTTGAC CTGTCTTACC 7140

AAGACATTCG ACCGCCTGAT AAACATCTAA AAGACTAATA TCCTTAAGGT CCTTGACAAT 7200

CTCTGTTCCG CCCGTTCCAC GCGCTACTGA AATCAGCTCT GCCTTCTTCA ACTGGGACAA 7260

GATCTTTCTG ATAATGACAG GATTGACCCC GACACTAGCA GCCAGAAAAT CACTGGTCAC 7320

CTTGCTTTCC TTCCCCTCGA GGGCAATGAT TATCAGCATA TGAGTCGCAA TGGTAAATCT 7380

ACTTGGAATT TGCATCCTCT TCTCCTTTTT ACGAGGCTAC CCTGCCTCTA CTCTTCTTTT 7440

TCTATTATTA TACCCTTTTT AGTTGTAATG TCAATCGTTA CCACTTTTCA ACCAGTCGTC 7500

TAACTCCCGA TCGCAGCCCT CTTTCTGAGC CAATTCTCTC AAAAATTCCT GATGATGAGT 7560

ATGGTGGATC CCATTGACCA GACTTTCATA GTAAACCTCA AAATAGGGAA GTCTCAGGTC 7620

TTTAGCCAGC TGCAATTCAG CTGCTACATC GTAGTCTACC CGTCGGAAGT CCATATCTAC 7680

CAGGCCTTTG TCATCAAACT CCAAAATCAT ATACTGGGCC CGCAAGTCCT TCCGTAGCTG 7740

AGCGTCCAAA AAGAAAGGTT GGCCAATCGA ACCCGGATTG ACAATCAATT GCCCACCAGT 7800

CCCGTAACGA AGCAACTGCT GGTGAATATG TCCATAAACA GCAATATCAC AGGGAGGATG 7860

AGTCACCAAG CGGTCAAACT CCTCTTGTTT GCCAGTATGA ATCAACTCTC GCCCCCAGTT 7920

CTTATCAGGC AGATGATGGC TAATTCCCAC CGTCAAATCC CCAAACTGAC GATGAATTTG 7980

AAGAGGTTGA TTGTGGAGCA CTTCAATTTC TTCTAGGGAA ATTTCCTCTA AAACATACTG 8040

GCACTGGCGC AAGAGATAGC GTTGACTGGG GCGAGTACTG TCCAATTCCT TACGGACACC 8100

ATGCCAAAGA CTGTCTTCCC AGTTTCCCAA AACTCTAGCC GTAATCGGTA GTTGATCCAA 8160

CAAGTCCAAA ATCCTTCTAC GCCCTGTCCC TGGCATGAGA ATATCTCCCA AAAGCCAGTA 8220

TTCATCCACT CCTATCTGCC GAGCATCTGC CAAAACAGCC TCCAAGGCGG TGGTATTTCC 8280

ATGAATATCT GAAAGAAGAG CTATTTTCGT CATATCCATC TCCTCGTTTT TTCTCTTGCA 8340

ATAAGTATAA CATAAAAAGT CACAGCTAGA GAAATCTAGC TTTTTTTGAT ATACTAGATA 8400

AAGATATTAG ACAAGAGGAA ACGAATGACC CCAAACAAAG AAGACTATCT AAAATGTATT 8460

TATGAAATTG GCATAGACCT GCATAAGATT ACCAACAAGG AAATTGCGGC TCGCATGCAA 8520

GTCTCTCCCC CTGCCGTAAC TGAAATGATC AAACGAATGA AAAGTGAAAA TCTCATCCTA 8580

AAGGACAAGG AATGTGGCTA TCTACTGACT GACCTCGGTC TCAAACTGGT CTCTGAGCTC 8640

TATCGTAAGC ACCGCTTGAT TGAAGTTTTT CTAGTTCATC ATTTAGACTA TACAAGTGAC 8700

CAGATTCACG AGGAAGCTGA GGTCTTGGAA CACACTGTCT CTGACCTGTT CGTGGAAAGA 8760
CTAGATAAAC TGCTAGGTTT CCCTAAAACC TGCCCCCACG GGGGAACTAT TCCTGCCAAG 8820
GGAGAACTAC TCGTTGAAAT CAATAACCTC CCACTAGCTG ATATCAAGGA AGCTGGCGCC 8880
TACCGCCTGA CTCGGGTGCA CGATAGTTTT GACATTCTCC ATTATCTGGA CAAGCACTCA 8940
CTTCACATCG GTGACCAGCT CCAAGTCAAG CAGTTTGATG GCTTCAGCAA TACCTTCACT 9000
ATCCTCAGTA ACGACGAGGA TTTACAAGTG AATATGGACA TTGCAAAACA ACTCTATGTC 9060
GAGAAAATCA ACTAATTTCT CAAGTCCCCT ACCAACCCTG AAAGTTTTAT TTTGGCTCTT 9120
TGTCAACTGT AGTGGGTTGA AGTCAGCTAA GCTCGAGAAA GGACAAATTT TGTCCTTTCT 9180
TTTTTGATAT TCAGAGCGAT AAAAATCCGT TTTTTGAAGT TTTCAAAGTT CCGAAAACCA 9240
AAGGCATTGC GCTTGATAAG TTTGATGAGA TTATTGGTCG CTTCCAGTTT GGCATTAGAA 9300
TAGTGTAGTT GAAGGGCGTT GACAATCTTT TCTTTATCTT TGAGGAAGGT TTTAAAGACA 9360
GTCTGAAAAA TAGGATGAAC CTGCTTTAGA TTGTCCTCAA TGAGTCCGAA AAATTTCTCC 9420
GGTTTCTTAT TCTGAAAGTG AAACAGCAAG AGTTGATAGA GCTGATAGTG GTGTTTCAAG 9480
TCTTGTGAAT AGCTCAAAAG CTTGTCTAAA ATCTCTTTAT TGGTTAAGTG CATACGAAAA 9540
GTAGGACGAT AAAATCGCTT ATCACTCAGT TTACGGCTAT CCTGTTGTAT GAGCTTCCAG 9600
TAGCGCTTGA TAGCCTTGTA TTCATGGGAT TTTCGATCCA ATTGGTTCAT AATTTGAACA 9660
CGCACACGAC TCATAGCACG GCTAAGATGT TGTACAATGT GAAAGCGATC CAACACGATT 9720
TTAGCATTCG GGAGTGAAAC AGTCTGGGAG ACTGTTTCAG CCTGAGCCTA GAAATTTGAA 9780
AGCGAAGCTG TTTAGCCAAG TCATAGTAAG GACTAAACAT ATCCATCGTA ATGATTTTCA 9840
CTTGACAACG AACGGCTCTA TCGTAGCGAA GAAAGTGATT TCGGATGACA GCTTGTGTTC 9900
TGCCTTCAAG AACAGTGATA ATATTAAGAT TATCAAAATC TTGCGCAATG AAACTCATCT 9960
TTCCCTTAGT GAAGGCATAC TCATCCCAAG ACATAATCTT TGGAAGCCGA GAAAAATCAT 10020
GCTCAAAGTG AAAGTCATTG AGCTTGCGAA TGACAGTTGA AGTTGAAATG GCCAGCTGAT 10080
GGGCAATATC AGTCATAGAA ATTTTTTCAA TTAACTTTTG AGCAATyTTT TGGTTGATGA 10140
TACGAGGGAT TTGGTGATTT TTCTTTACCA GGGGAGTCTC AGCAACCATC ATTTTTGAAC 10200
AGTGATAGCA CTTGAAACGA CGCTTTCTAA GGAGAATTCT AGAAGGCATA CCAGTCGTTT 10260
CAAGATAAGG AATTTTAGAA GGTTTTTGAA AGTCATATTT CTTCAATTGG TTTCCGCACT 10320
CAGGGCAAGA TGGGGCGTCG TAGTCCAGTT TGGCGATGAT TTCCTTGTGT GTATCCTTAT 10380
TGATGATGTC TAAAATCTGG ATATTAGGGT CTTTAATGTC TAGTAATTTT GTGATAAAAT 10440

GTAATTGTTC CATATGATTC TTTCTAATGA GTTGTTTTGT CGCTTTTCAT TATAGGTCAT 10500

ATGGGACTTT TTTTCTACAA TAAAATAGGC TCCATAATAT CTATAGTGGA TTTACCCACT 10560

ACAAATATTA TAGAACCGTA AAAATAGAAG GAGATAGCAG GTTTTCAAGC CTGCTATCTT 10620

TTTTTGATGA CATTCAGGCT GATACGAAAT CATAAGAGGT CTGAAACTAC TTTCAGAGTA 10680

GTCTGTTCTA TAAAATATAG TAGATTGAAA TAAGATGTGA ACAACTCTAT CAGGAAAGTC 10740

AAATTAATTT ATAGAATTAT TTTAGCAGTC AAGGTGTACT GTTATAGATT CAATATATTA 10800

TATGACTATT AACCTTGTCT TCTCCTAAAA TTGACTTTCT TGTTTTCTTA TCTTGTCCAC 10860

TCGAAACAAG TATTGTAAGA ATTTGATTAT TTTTGAAAGT ACTTTTAATA TACTTGATAT 10920

AGTTAAAAAA GATTTGAAAC TAAATTCCAA ATTAGAAAAA GACTTGAAAT ACTAAAAAAA 10980

AAAAAGTATA CTCTAATTGA AAACGGTAAC AAAACTAATT TAGAGAATGA AATATAGAGT 11040

ATTTCTCTCT TAAAAGTTTT TGGTGAAACG AGATGTAGAA AGGAGATTTA GCCAAAGAGT 11100

CTATTAGTGC TAGAATAATA GATTAGAATT ATTTTAGAAA AACGAAGTGA GCAGCTTATA 11160

AATTCAAGTC CCCAAATAGA TTCATACTAG TATCTTTTGC AAAAAATAAA GGGCGACTTC 11220

CTTCATGAAT ATCAATTTCA TCTATAAGGA AGGTAGCTAA TTGAACTAAC TTATTTATTC 11280

TGTTTGTCGC TAGAAAAATC AGACCTCCTT GTGAAGATTG AGGAGATACT TAATGAAAAT 11340

CAAAGAAGAA ACTAGCAAGC TAGTAGCAGA TTGCCCAAAA CACCGCTTTG AGGTTGTAGA 11400

TAAGACTGAC CTATATAATC CAAGGTGAAG CGACTGTGGT TTGAAGAGAT TTTCAAAGAG 11460

TATAGGCTAG AGAGTAGTGT TTTTATGTCC TTCTAGTAGA AAATGCTAGA CAGAAGAATG 11520

GGGAACTTGG ATAGGAAAAA TAGATTGAGA AAGGAGGTTA GAAGAGATGA TTATTACAAA 11580

AATTAGCCGT TTAGGAACTT ATGTGGGAGT AAATCCACAT TTTGCAACAT TAATAGATTT 11640

TCTAGAAAAA ACAGGACTAG AAAATTTAAC AGAAGGTTCG ATTGCTATCG ATGGTAATCG 11700

ATTGTTTGGG AATTGCTTTA CTTATCTAGC AGATGGTCAA GCAGGGGCTT TCTTTGAAAC 11760

CCACCAAAAA TATTTGGATA TTCATTTAGT TTTGGAAAAC GAAGAAGCCA TGGCTGTTAC 11820

ATCGCCGGAA AATGTAAGCG TTACCCAAGA ATATGATGAA GAGAAAGATA TTGAATTATA 11880

CACAGGGAAA GTGGAACAGT TGGTTCATTT GAGAGCTGGC GAATGCCTCA TCACTTTTCC 11940

AGAAGATTTA CATCAACCCA AGGTTCGTAT AAATGATGAA CCTGTGAAAA AAGTTGTCTT 12000

TAAAGTTGCG ATTTCTTAAT GTAGAAAGAG AAGAACGATG AAAAAAATGA GAAAGTTTTT 12060

ATGTCTAGCT GGAATTGCGC TAGCGGCTGT TGCCTTGGTA GCTTGTTCAG GAAAAAAAGA 12120

AGCTACAACT AGTACTGAAC CACCAACAGA ATTATCTGGT GAGATTACAA TGTGGCACTC 12180

CTTTACTCAA GGACCCCGTT TAGAAAGTAT TCAAAAATCA GCAGATGCTT TCATGCAAAA 12240

GCATCCAAAA ACGAAAATCA AGATTGAAAC ATTTTCTTGG AATGACTTCT ATACTAAATG 12300

GACTACAGGT TTAGCAAATG GAAATGTGCC AGATATCAGT ACAGCTCTTC CTAACCAAGT 12360

AATGGAAATG GTCAACTCAG ATGCTTTGGT TCCGCTAAAT GATTCTATCA AGCGTATTGG 12420

ACAAGATAAA TTTAACGAAA CTGCCTTAAA TGAAGCAAAA ATCGGAGATG ATTACTACTC 12480

TGTTCCTCTT TATTCACATG CACAAGTCAT GTGGGTTAGA ACAGATTTGT TAAAAGAACA 12540

TAATATTGAG GTTCCTAAAA CTTGGGATCA ACTCTATGAA GCTTCTAAAA AATTGAAAGA 12600

AGCTGGAGTT TATGGCTTGT CTGTTCCGTT TGGAACAAAT GACTTAATGG CAACACGTTT 12660

CTTGAACTTC TACGTACGTA rTGGTGGAGG AAGCCTCTTA ACAAAAGATC TTAAAGCAGA 12720

CTTGACAAGC CAACTTGCTC AAGATGGTAT TAAATACTGG GTTAAATTGT ATAAAGAAAT 12780

CTCACCTCAA GATTCTTTGA ACTTTAATGT CCTTCAACAA GCTACCTTGT TCTATCAAGG 12840

AAAAACAGCA TTTGACTTTA ACTCTGGCTT CCATATCGGA GGAATTAATG CCAACAGTCC 12900

TCAATTGATT GATTCGATTG ATGCTTATCC TATTCCAAAA ATCAAAGAGT CTGATAAAGA 12960

CCAAGGAATT GAAACCTCAA ACATTCCAAT GGTTGTTTGG AAAAATTCAA AACATCCAGA 13020

AGTTGCTAAA GCATTCTTAG AAGCACTTTA TAATGAAGAA GACTACGTTA AATTCCTTGA 13080

TTCAACTCCA GTAGGTATGT TGCCAACTAT TAAGGGGATT AGCGATTCTG CAGCCTATAA 13140

AGAAAATGAA ACTCGTAAGA AATTTAAACA TGCTGAAGAA GTAATTACTG AAGCTGTTAA 13200

AAAAGGTACT GCTATTGGTT ATGAAAATGG GCCAAGTGTA CAAGCTGGTA TGTTGACTAA 13260

CCAACACATT ATTGAACAAA TGTTCCAAGA TATCATTACA AATGGAACAG ATCCTATGAA 13320

AGCAGCAAAA GAAGCAGAAA AACAATTAAA TGATTTATTT GAGGCTGTTC AGTAGATGTA 13380

AAAGACTAGA AAATAGGTGG GATAGTGAGC TGAAAAGCTC TAGCCCAATC TTGTAAAAGA 13440

AGGGAGAAGG AGAATGGTTA AAGAACGTAA TTTAACTCGC TGGATATTTG TTTTGCCAGC 13500

TATGATTATC GTAGGATTAC TCTTTGTTTA TCCGTTTTTC TCGAGTATTT TTTATAGCTT 13560

TACCAATAAG CATTTGATTA TGCCTAATTA TAAATTTGTT GGTTTGGCTA ACTATAAAGC 13620

TGTGCTATCA GATCCCAACT TCTTTAATGC GTTCTTTAAT TCAATTAAGT GGACCGTTTT 13680

CTCATTAGTT GGTCAAGTTT TAGTAGGGTT TGTATTGGCT TTAGCTCTTC ACAGAGTACG 13740

CCACTTCAAG AAATTATATA GGACATTATT GATTGTTCCT TGGGCATTTC CTACCATCGT 13800

TATTGCCTTC TCTTGGCAGT GGATTCTAAA CGGGGTTTAT GGCTACTTAC CTAATCTAAT 13860

CGTAAAATTA GGTTTAATGG AACATACACC TGCATTTTTG ACAGATAGTA CATGGGCATT 13920

CCTATGTTTG GTGTTTATCA ACATTTGGTT TGGAGCACCA ATGATTATGG TTAATGTGCT 13980

TTCAGCTTTG CAAACAGTAC CAGAAGAACA ATTTGAGGCT GCTAAGATAG ATGGTGCTTC 14040

AAGTTGGCAG GTGTTCAAGT TTATCGTCTT TCCACATATT AAAGTGGTTG TAGGACTTCT 14100

AGTTGTTTTG AGAACTGTAT GGATCTTTAA TAACTTTGAC ATTATCTACC TCATTACTGG 14160

TGGTGGACCA GCCAATGCTA CAACGACGCT TCCAATTTTT GCTTACAACC TGGGCTGGGG 14220

AACTAAATTG TTGGGTCGTG CTTCAGCAGT TACAGTACTG CTCTTTATCT TCTTGGTGGC 14280

GATTTGCTTT ATCTACTTTG CTATCATCAG TAAGTGGGAA AAGGAGGGTA GAAAATAATG 14340

AAGAAGAAAT CCAGTATTTA TTTAGATATT CTCTCACATG TACTTTTAGT TGGTGCGACC 14400

ATCGTTGCAG TTTTCCCATT GGTATGGATT ATCATATCTT CTGTCAAAGG GAAAGGGGAA 14460

TTAACTCAGT ATCCAACACG ATTTTGGCCT GAACAGTTTA CATTAGATTA TTTCACTCAT 14520

GTTATCAACG ATTTGCACTT CATTGATAAC ATTCGAAACA GTTTAATCAT TGCCTTGGCT 14580

ACAACCCTTA TTGCGATTAT TATTTCTGCT ATGGCAGCCT ATGGTATTGT TCGATTCTTT 14640

CCTAAATTGG GAGCAATCAT GTCGAGACTA CTCGTCATTA CCTACATTTT CCCACCAATT 14700

TTGTTAGCAA TTCCCTATTC AATTGCCATT GCTAAAGTTG GGTTAACAAA TAGTTTATTT 14760

GGCTTGATGA TGGTTTATCT ATCTTTTAGT GTTCCATATG CAGTTTGGCT CTTAGTTGGA 14820

TTTTTCCAAA CAGTTCCAAT TGGAATTGAA GAAGCGGCTA GAATTGATGG TGCAAATAAA 14880

TTTGTTACGT TTTATAAAGT TGTGCTACCG ATTGTAGCAC CAGGTATTGT AGCAACAGCT 14940

ATTTATACAT TTATCAATGC TTGGAATGAA TTCCTGTATG CCTTGATTTT GATTAACAAT 15000

ACAGGAAAGA TGACAGTAGC AGTAGCCCTT CGTTCACTTA ATGGTTCAGA AATACTAGAC 15060

TGGGGAGATA TGATGGCAGC GTCTGTTATT GTAGTTCTTC CATCAATTAT TTTCTTCTCT 15120

ATCATCCAAA ATAAGATTGC AAGTGGATTA TCAGAAGGAT CTGTGAAGTA GACGAAAGAA 15180

GGAAAAAAAT GAATAAAAGA GGTCTTTATT CAAAACTAGG AATTTCCGTT GTAGGCATTA 15240

GTCTTTTAAT GGGAGTCCCC ACTTTGATTC ATGCGAATGA ATTAAACTAT GGTCAACTGT 15300

CCATATCTCC TATTTTTCAA GGAGGTTCAT ATCAACTGAA CAATAAGAGT ATAGATATCA 15360

GCTCTTTGTT ATTAGATAAA TTGTCTGGAG AGAGTCAGAC AGTAGTAATG AAATTTAAAG 15420

CAGATAAACC AAACTCTCTT CAAGCTTTGT TTGGCCTATC TAATAGTAAA GCAGGCTTTA 15480

AAAATAATTA CTTTTCAATT TTCATGAGAG ATTCTGGTGA GATAGGTGTA GAAATAAGAG 15540

ACGCCCAAAA GGGAATAAAT TATTTATTTT CCAGACCAGC TTCATTATGG GGAAAACATA 15600

AAGGACAGGC AGTTGAAAAT ACACTAGTAT TTGTATCTGA TTCTAAAGAT AAAACATACA 15660

CAATGTATGT TAATGGAATA GAAGTGTTCT CTGAAACAGT TGATACATTT TTGCCAATTT 15720

CAAATATAAA TGGTATAGAT AAGGCAACAC TAGGAGCTGT TAATCGTGAA GGTAAGGAAC 15780

ATTACCTCGC AAAAGGAAGT ATTGATGAAA TCAGTCTATT TAACAAAGCA ATTAGTGATC 15840

AGGAAGTTTC AACTATTCCC TTGTCAAATC CATTTCAGTT AATTTTCCAA TCAGGAGATT 15900

CTACTCAAGC TAACTATTTT AGAATACCGA CACTATATAC ATTAAGTAGT GGAAGAGTTC 15960

TATCAAGTAT TGATGCACGT TATGGTGGGA CTCATGATTC TAAAAGTAAG ATTAATATTG 16020

CCACTTCTTA TAGTGATGAT AATGGGAAAA CGTGGAGTGA GCCAATTTTT GCTATGAAGT 16080

TTAATGACTA TGAGGAGCAG TTAGTTTACT GGCCACGAGA TAATAAATTA AAGAATAGTC 16140

AAATTAGTGG AAGTGCTTCA TTCATAGATT CATCCATTGT TGAAGATAAA AAATCTGGGA 16200

AAACGATATT ACTAGCTGAT GTTATGCCTG CGGGTATTGG AAATAATAAT GCAAATAAAG 16260

CCGACTCAGG TTTTAAAGAA ATAAATGGTC ATTATTATTT AAAACTAAAG AAGAATGGAG 16320

ATAACGATTT CCGTTATACA GTTAGAGAAA ATGGTGTCGT TTATAATGAA ACAACTAATA 16380

AACCTACAAA TTATACTATA AATGATAAGT ATGAAGTTTT GGAGGGAGGA AAGTCTTTAA 16440

CAGTCGAACA ATATTCGGTT GATTTTGATA GTGGCTCTTT AAGAGAAAGG CATAATGGAA 16500

AACAGGTTCC TATGAATGTT TTCTACAAAG ATTCGTTATT TAAAGTGACT CCTACTAATT 16560

ATATAGCAAT GACAACTAGT CAGAATAGAG GAGAGAGTTG GGAACAATTT AAGTTGTTGC 16620

CTCCGTTCTT AGGAGAAAAA CATAATGGAA CTTACTTATG TCCCGGACAA GGTTTAGCAT 16680

TAAAATCAAG TAACAGATTG ATTTTTGCAA CATATACTAG TGGAGAACTA ACCTATCTCA 16740

TTTCTGATGA TAGTGGTCAA ACATGGAAGA AATCCTCAGC TTCAATTCCG TTTAAAAATG 16800

CAACAGCAGA AGCACAAATG GTTGAACTGA GAGATGGTGT GATTAGAACA TTCTTTAGAA 16860

CCACTACAGG TAAGATAGCT TATATGACTA GTAGAGATTC TGGAGAAACA TGGTCGAAAG 16920

TTTCGTATAT TGATGGAATC CAACAAACTT CATATGGCAC ACAAGTATCT GCAATTAAAT 16980

ACTCTCAATT AATTGATGGA AAAGAAGCAG TCATTTTGAG TACACCAAAT TCTAGAAGTG 17040

GCCGCAAGGG AGGCCAATTA GTTGTCGGTT TAGTCAATAA AGAAGATGAT AGTATTGATT 17100

GGAAATACCA CTATGATATT GATTTGCCTT CGTATGGTTA TGCCTATTCT GCGATTACAG 17160

AATTGCCAAA TCATCACATA GGTGTACTGT TTGAAAAATA TGATTCGTGG TCGAGAAATG 17220

AATTGCATTT AAGCAATGTA GTTCAGTATA TAGATTTGGA AATTAATGAT TTAACAAAAT 17280

AAAGGAGAAA AACATGGTTA AATACGGTGT TGTTGGAACA GGGTATTTTG GAGCTGAATT 17340

GGCTCGCTAC ATGCAAAAGA ATGATGGAGC AGAGATTACT CTTCTCTATG ATCCAGATAA 17400

TGCAGAGGCG ATTGCAGAAG AATTGGGAGC AAAAGTAGCA AGTTCCTTAG ATGAGTTGGT 17460

TTCTAGCGAT GAAGTAGATT GTGTTATCGT CGCAACTCCA AATAATCTTC ATAAGGAACC 17520

GGTTATTAAG GCTGCACAGC ATGGTAAAAA TGTTTTCTGT GAAAAACCAA TTGCGCTTTC 17580

TTATCAAGAT TGTCGCGAGA TGGTAGATGC GTGTAAAGAA AACAATGTAA CCTTTATGGC 17640

AGGACATATT ATGAATTTCT TTAATGGTGT TCATCATGCA AAAGAACTCA TTAATCAAGG 17700

AGTTATCGGA GACGTTCTAT ATTGTCATAC AGCTCGTAAT GGTTGGGAAG AACAACAACC 17760

GTCAGTATCA TGGAAAAAAA TTCGTGAAAA ATCAGGTGGT CACTTGTATC ACCACATCCA 17820

TGAATTGGAT TGCGTTCAAT TCCTTATGGG GGGCATGCCT GAAACTGTAA CCATGACAGG 17880

TGGAAATGTG GCCCATGAAG GTGAACATTT CGGTGATGAA GATGATATGA TTTTTGTCAA 17940

TATGGAATTT TCTAATAAGC GTTTTGCCTT GTTAGAATGG GGTTCAGCTT ATCGTTGGGG 18000

TGAACATTAT GTCTTAATCC AAGGAAGCAA AGGTGCCATC CGCTTAGACT TATTCAACTG 18060

TAAAGGAACT CTTAAGCTAG ATGGGCAAGA AAGCTATTTC TTGATTCACG AATCGCAAGA 18120

AGAAGATGAT GATCGGACTC GTATCTATCA TAGTACAGAG ATGGATGGAG CAATTGCTTA 18180

TGGTAAACCA GGTAAACGTA CTCCATTATG GCTATCATCT GTCATTGATA AAGAAATGCG 18240

CTATCTGCAT GAGATTATGG AAGGAGCTCC AGTATCAGAA GAATTTGCAA AACTTTTGAC 18300

AGGTGAAGCT GCCCTAGAAG CAATTGCTAC TGCAGATGCT TGTACCCAGT CTATGTTTGA 18360

AGATCGCAAA GTAAAATTGT CAGAAATTGT AAAATAAATT TTGGTATTCT CCTATTTATA 18420

GGTCGACTTG CTCCTCTGAA AGTACTTTTA GAGGAGCTGT TTGACTTTGC TAGTTTTTGA 18480

AACTGAAATC TATTATACTA CAAACTATTG AAAGCGTTTT AATTTTAAGG TATAATAATC 18540

TCATAGAAAT AAAGAAAAGG AGGAAAGAGG ATGCCACAGA TTAGCAAAGA AGCCTTGATT 18600

GAGCAAATCA AAGATGGAAT CATCGTTTCT TGTCAGGCTC TTCCTCATGA ACCGCTTTAT 18660

ACAGAAGCGG GAGGGGTGAT TCCCTTGCTG GTCAAAGCGG CTGAGCAAGG TGGAGCAGTC 18720

GGTATCCGAG CAAACAGTGT TCGCGATATC AAGGAAATTA AGGAAGTCAC TAAACTTCCA 18780

ATCATTGGGA TTATCAAACG TGATTATCCA CCTCAGGAAC CCTTCATCAC GGCTACTATG 18840

AAAGAAGTTG ATGAATTGGC AGAACTGGAC ATCGAGGTGA TTGCTCTGGA TTGTACCAAG 18900

CGTGAACGCT ACGATGGTTT GGAAATTCAA GAGTTCATTC GTCAGGTTAA GGAGAAATAT 18960

CCTAATCAGC TTTTGATGGC TGATACTAGT ATCTTCGAAG AAGGGCTAGC AGCTGTAGAA 19020

GCAGGAATTG ACTTTGTCGG AACAACCTTA TCAGGCTACA CATCCTACAG TCCAAAAGTA 19080

GACGGTCCAG ATTTTGAATT GATTAAGAAA CTCTGTGATG CTGGTGTAGA TGTCATTGCA 19140

GAAGGAAAAA TTCATACACC AGAACAAGCC AAACAAATCC TTGAATATGG AGTGCGAGGC 19200

ATCGTTGTTG GTGGCGCCAT TACTAGACCA AAAGAGATTA CAGAACGCTT CGTTGCTAGT 19260

CTTAAATAAG ATGTGAGGGG GAGTTTTATG TTTAAAGTTT TACAAAAAGT TGGAAAAGCT 19320

TTTATGTTAC CTATAGCTAT ACTTCCTGCA GCAGGTCTAC TTTTGGGGAT TGGTGGTGCA 19380
CTTTCAAACC CAACCACGAT AGCAACTTAT CCAATACTAG ACAATAGTAT TTTTCAATCA 19440
ATATTCCAAG TAATGAGCTC TGCAGGAGAG GTTGTATTCA GTAATTTGTC ACTACTTCTC 19500
TGTGTGGGAT TATGTATTGG CTTAGCGAAA CGAGATAAAG GAACCGCTGC GTTAGCAGGA 19560
GTAACTGGTT ACTTAGTTAT GACTGCAACG ATCAAAGCTT TGGTAAAACT TTTTATGGCA 19620
GAAGGATCTG CAATTGATAC TGGAGTTATT GGAGCATTAG TTGTCGGAAT AGTTGCCGTA 19680
TATTTGCACA ACCGATATAA CAATATTCAA TTACCTTCCG CTTTAGGATT CTTTGGAGGT 19740
TCACGCTTCG TTCCTATTGT TACATCGTTC TCTTCTATCT TGATTGGCTT TGTCTTCTTT 19800
GTTATTTGGC CACCTTTCCA ACAACTTCTT GTTTCTACAG GTGGATATAT TTCTCAGGCG 19860
GGTCCAATTG GAACTTTTCT ATATGGATTT TTAATGAGAC TTTCTGGAGC AGTAGGCTTA 19920
CATCATATAA TTTACCCTAT GTTTTGGTAT ACTGAACTTG GTGGTGTTGA AACTGTTGCA 19980
GGACAAACAG TGGTTGGAGC TCAAAAAATA TTTTTTGCTC AATTAGCCGA TTTGGCCCAT 20040
TCTGGATTAT TTACAGAAGG AACAAGGTTT TTTGCAGGTC GTTTCTCAAC AATGATGTTC 20100
GGTTTACCGG CTGCCTGTTT AGCGATGTAC CATAGTGTTC CTAAAAATCG TCGTAAAAAA 20160
TACGCGGGTT TGTTTTTTGG AGTTGCTTTA ACATCTTTTA TTACCGGTAT TACAGAACCA 20220
ATTGAATTTA TGTTTCTATT CGTCAGTCCG GTTCTATATG TTGTTCACGC ATTCCTTGAT 20280
GGTGTTAGCT TCTTTATTGC AGACGTCTTA AATATTTCAA TAGGAAACAC ATTTTCAGGA 20340
GGTGTAATCG ATTTCACTTT ATTTGGAATT TTGCAGGGGA ACGCTAAGAC GAATTGGGTT 20400
CTTCAGATTC CATTTGGACT TATTTGGAGT GTTTTGTATT ATATTATTTT TAGATGGTTC 20460
ATTACTCAAT TCAACGTTCT AACGCCAGGG CGAGGAGAAG AAGTAGATTC TAAAGAAATT 20520
TCTGAATCCG CAGATTCAAC TTCAAATACT GCAGATTATT TAAAACAGGA TAGCCTACAA 20580
ATTATCAGAG CCTTGGGTGG ATCAAATAAT ATAGAAGATG TAGATGCTTG TGTGACACGT 20640
TTACGTGTAG CTGTAAAAGA AGTTAATCAA GTTGATAAAG CACTTTTAAA ACAAATTGGT 20700
GCAGTTGATG TCTTAGAAGT GAAGGGTGGC ATTCAAGCAA TCTATGGAGC AAAAGCAATC 20760
TTATATAAAA ATAGTATTAA TGAAATTTTA GGTGTAGATG ATTAAGTACT TACTGACTTA 20820
ATAAAAAACA GAGGAGAGTG ATGGATGAGT AGGATGAAAT GAAATCGCAT ACAAGAAATA 20880
AAGAACTCAT TATCCAAGTT GGATACGCTT ATTACATAGG AGAATACAAA TGAAATTTAG 20940
AAAATTAGCT TGTACAGTAC TTGCGGGTGC TGCGGTTCTT GGTCTTGCTG CTTGTGGCAA 21000
TTCTGGCGGA AGTAAAGATG CTGCCAAATC AGGTGGTGAC GGTGCCAAAA CAGAAATCAC 21060

TTGGTGGGCA TTCCCAGTAT TTACCCAAGA AAAAACTGGT GACGGTGTTG GAACTTATGA 21120

AAAATCAATC ATCGAAGCGT TTGAAAAAGC AAACCCAGAT ATAAAAGTGA AATTGGAAAC 21180

CATCGACTTC AAGTCAGGTC CTGAAAAAAT CACAACAGCC ATCGAAGCAG GAACAGCTCC 21240

AGACGTACTC TTTGATGCAC CAGGACGTAT CATCCAATAC GGTAAAAACG GTAAATTGGC 21300

TGAGTTGAAT GACCTCTTCA CAGATGAATT TGTTAAAGAT GTCAACAATG AAAACATCGT 21360

ACAAGCAAGT AAAGCTGGAG ACAAGGCTTA TATGTATCCG ATTAGTTCTG CCCCATTCTA 21420

CATGGCAATG AACAAGAAAA TGTTAGAAGA TGCTGGAGTA GCAAACCTTG TAAAAGAAGG 21480

TTGGACAACT GATGATTTTG AAAAAGTATT GAAAGCACTT AAAGACAAGG GTTACACACC 21540

AGGTTCATTG TTCAGTTCTG GTCAAGGGGG AGACCAAGGA ACACGTGCCT TTATCTCTAA 21600

CCTTTATAGC GGTTCTGTAA CAGATGAAAA AGTTAGCAAA TATACAACTG ATGATCCTAA 21660

ATTCGTCAAA GGTCTTGAAA AAGCAACTAG CTGGATTAAA GACAATTTGA TCAATAATGG 21720

TTCACAATTT GACGGTGGGG CAGATATCCA AAACTTTGCC AACGGTCAAA CATCTTACAC 21780

AATCCTTTGG GCACCAGCTC AAAATGGTAT CCAAGCTAAA CTTTTAGAAG CAAGTAAGGT 21840

AGAAGTGGTA GAAGTACCAT TCCCATCAGA CGAAGGTAAG CCAGCTCTTG AGTACCTTGT 21900

AAACGGGTTT GCAGTATTCA ACAATAAAGA CGACAAGAAA GTCGCTGCAT CTAAGAAATT 21960

CATCCAGTTT ATCGCAGATG ACAAGGAGTG GGGACCTAAA GACGTAGTTC GTACAGGTGC 22020

TTTCCCAGTC CGTACTTCAT TTGGAAAACT TTATGAAGAC AAACGCATGG AAACAATCAG 22080

CGGCTGGACT CAATACTACT CACCATACTA CAACACTATT GATGGATTTG CTGAAATGAG 22140

AACACTTTGG TTCCCAATGT TGCAATCTGT ATCAAATGGT GACGAAAAAC CAGCAGATGC 22200

TTTGAAAGCC TTCACTGAAA AAGCGAACGA AACAATCAAA AAAGCTATGA AACAATAGTC 22260

CTTAGTTATT CTATAAAAAG TAGTTTTTTA AAGAACCTAA GAGTGTATAC CCCCTTTTCC 22320

CTCTACACAG ATAGTGTAAG AAAAGGGGGC TTTTGTTTAA AATGTAAGAA ACTGTCACGA 22380

AATTAAAATG AAGTTCTTAC ATAAGCGAAT CATAAAAAAT TTCATTTTGA TTTTAAAACA 22440

GTTCAAGAAA GTCAAAAAAT TATTCTATTT GAAAGAGAGG TGCCGACTGT GAAAGTCAAT 22500

AAAATCCGTA TGCGGGAAAC AGTGATTTCC TACGCTTTCC TAGCACCAGT ATTATTCTTC 22560

TTTGTCATCT TTGTGTTGGC TCCGATGGTG ATGGGCTTCA TTACAAGTTT CTTTAACTAC 22620

TCAATGACTA AATTTGAGTT TGTAGGCTTG GATAACTATA TCCGTATGTT TAAAGATCCT 22680

GTCTTTACAA AATCTCTGAT TAACACAGTT ATTTTGGTTA TTGGATCTGT ACCAGTTGTT 22740

GTTCTATTCT CACTCTTTGT AGCATCTCAG ACCTATCATC AAAATGTCAT TGCCAGATCC 22800

TTCTACCGTT TCGTCTTCTT CCTTCCTGTT GTAACGGGTA GTGTTGCCGT GACAGTTGTT 22860

TGGAAATGGA TTTATGACCC ACTATCAGGG ATTCTAAACT TTGTCCTTAA GTCCAGCCAC 22920
ATCATCAGCC AAAACATTTC TTGGTTGGGA GATAAAAACT GGGCATTGAT GGCGATTATG 22980
ATTATTCTCT TGACCACTTC AGTTGGTCAG CCCATCATCC TTTATATCGC TGCCATGGGG 23040
AATATTGACA ATTCACTGGT TGAAGCGGCG CGTGTTGATG GTGCAACTGA GTTTCAAGTT 23100
TTTTGGAAGA TTAAATGGCC AAGCCTTCTT CCAACAACTC TTTATATTGC AATCATCACA 23160
ACAATTAACT CATTCCAGTG TTTCGCCTTG ATTCAGCTTT TGACATCTGG TGGTCCAAAC 23220
TACTCAACAA GTACCTTGAT GTACTACCTT TACGAAAAAG CCTTCCAATT GACAGAATAC 23280
GGCTATGCCA ACACAATTGG TGTCTTCTTG GCAGTCATGA TTGCTATCGT AAGCTTTGTT 23340
CAATTTAAAG TACTTGGAAA CGACGTAGAA TACTAAAGAA AGGAGACAGC TATGCAATCT 23400
ACAGAAAAAA AACCATTAAC AGCCTTTACT GTTATTTCAA CAATCATTTT GCTCTTGTTG 23460
ACTGTGCTGT TCATCTTTCC ATTCTACTGG ATTTTGACAG GGGCATTCAA ATCACAACCT 23520
GATACAATTG TTATTCCTCC TCAGTGGTTC CCTAAAATGC CAACCATGGA AAACTTCCAA 23580
CAACTCATGG TGCAGAACCC TGCCTTGCAA TGGATGTGGA ACTCAGTATT TATCTCATTG 23640
GTAACCATGT TCTTAGTTTG TGCAACCTCA TCTCTAGCAG GTTATGTATT GGCTAAAAAA 23700
CGTTTCTATG GTCAACGCAT TCTATTTGCT ATCTTTATCG CTGCTATGGC GCTTCCAAAA 23760
CAAGTTGTCC TTGTACCATT GGTACGTATC GTCAACTTCA TGGGAATCCA TGATACTCTC 23820
TGGGCAGTTA TCTTGCCTTT GATTGGATGG CCATTCGGTG TCTTCCTCAT GAAACAGTTC 23880
AGTGAAAATA TCCCTACAGA GTTGCTTGAA TCAGCTAAAA TCGACGGTTG TGGTGAGATT 23940
CGTACCTTCT GGAGTGTAGC CTTCCCGATT GTGAAACCAG GGTTTGCAGC CCTTGCAATC 24000
TTTACCTTCA TCAATACTTG GAATGACTAC TTCATGCAAT TGGTAATGTT GACTTCACGT 24060
AACAATTTGA CCATCTCACT TGGGGTTGCG ACCATGCAGG CTGAAATGGC AACCAACTAT 24120
GGTTTGATTA TGGCAGGAGC TGCCCTTGCT GCTGTTCCAA TCGTCACAGT CTTCCTAGTC 24180
TTCCAAAAAT CCTTCACACA GGGTATTACT ATGGGAGCGG TCAAAGGATA ATACTCTGCG 24240
AAAATCTCTT CAAACTACGT CAGCTTCACC TTGCCATACT TAAGTATTGC CTGCGGTTAG 24300
CTTCCTAGTT TGTTCTTCAA TTTTCATTGA GTATAGGAAA ATCAATCTAT CAAGATACAG 24360
AAGTATATTT TATAGATTTA GAGAATATAG AGGTTATAAG TGTCTACAAA ATGGAGGGTA 24420
TGCAGTTACT TTATGAAGTT TTGTCAGACA CTTATAAACT TAAGAATGGT TTTAGTTAAC 24480
TATCAGAAAC GAAGGAAAGA GTATGATTTT TGACGATTTG AAAAACATCA CCTTTTACAA 24540
AGGGATTCAT CCTAATTTAG ACAAGGCTAT CGACTATCTC TACCAACATC GTAAGGATTC 24600

TTTCGAATTA GGAAAGTATG ATATTGATGG AGATAAAGTC TTTCTAGTTG TTCAGGAAAA 24660
TGTCCTCAAT CAAGCTGAAA ATGATCAATT TGAGTATCAT AAGAACTATG CAGATTTGCA 24720
TTTGCTGGTA GAAGGACATG AATATTCGAG CTACGGTTCA CGTATCAAAG ACGAGGCAGT 24780
AGCATTCGAC GAAGCGAGTG ACATTGGCTT TGTTCATTGT CATGAACACT ACCCACTCTT 24840
GTTGGGTTAT CACAATTTTG CGATTTTCTT CCCAGGTGAG CCACATCAGC CAAATGGTTA 24900
TGCAGGCATG GAAGAAAAGG TTCGAAAATA TCTCTTTAAA ATTTTGATTG ATTAAAAATA 24960
GGATGAATTG TTTTTTTGTA AAGCTTTGAT AATACTCTAC CATGAAATTG ATCTTTGTGA 25020
GGTAGAGAAA TGAGAATAAA ATATTTAAAA ATTGGTATCT TCTAAGTATG CTGCAAGAGC 25080
TAGTTTCTTA GATGGACAGG GGATTACAGT TGATGAGATG GCTTGGATAA TTAGGGGCAT 25140
TGTGAATGCA TTGATTGGTA GATACATAAA ATTAGGTACT TATGCGGCTA AGTATGGTAT 25200
TAGTATGGCA CGCTCGATCT TAAGTAGGGT AGCTGCAACT GCAGCAGCAA GAGTAGGATT 25260
ACTGACCAAG ATTTCTGGAT GGATTTTACG AGTAGCTGTG AATGTAGCTG ATGTATATGG 25320
TAATTTTGCC AACAATATTG CTGCAGCTTG GGATGCATAT GATAAAATTC CTAACAATGG 25380
TCGTATAAAC TTTTAAAATG CGAGAATGAA AGCACTTTGT ATTTTTTTAT TGAATATGTT 25440
AGCTTGGACA GTGCTTGCAA TGATAATTCG TGGAGGGCTA GATGGATTTG ATAGGCATAC 25500
TTGGAGTACT ATTTTAATTG CGTCGCTGTT CGGGGTATAT GATTATAAGC CCATAGATAA 25560
AAATAGAAAA AAGTCCAAAA GAAAAAATAG ATTTGTTCAT GGTAGGGACT TATGAAAGCT 25620
TTACTGACAA AAAAGAAAAC AGTTTACAAA GAAAAATGAT GGAGGAGCAA ACATGGCACA 25680
AAAAGGAGTA AGCCTTATCA AGGCAGCATT TGATACAGAT AACTTTCTCA TGCGTTTTAG 25740
TGAGAAGGTC TTGGACATCG TGACAGCCAA TCTTCTTTTT GTCGTCTCTT GTTTACCCAT 25800
CGTGACGATT GGAGTGGCTA AAATCAGCCT CTACGAGACC ATGTTCGAAG TTAAGAAGAG 25860
CAGACGGGTG CCTGTTTTTA AAATCTATCT AAGATCTTTC AAGCAAAATC TGAAACTAGG 25920
TCTTCAGCTG GGTTTAATGG AGTTAGGAAT TGTGTTTCTT ACCCTTTCAG ATCTCTATCT 25980
TTTCTGGGGT CAAACAGCTC TGCCCTTCCA ATTGCTGAAA GCCATTTGTT TAGGTATTCT 26040
GATTTTTCTT ACTATCGTGA TGCTGGCTAG TTACCCTATC GCGGCACGTT ATGACCTATC 26100
TTGGAAAGAA ATTCTTCAAA AAGGATTGAT GTTGGCTAGT TTTAACTTTC CTTGGTTCTT 26160
CCTCATGTTA GCCATTCTTG TCCTCATTGT GATGGTTCTT TATCTGTCCG CCTTCAGTCT 26220
ACTCTTAGGT GGCTCAGTCT TCCTACTTTT TGGGTTTGGA CTATTGGTCT TTATCCAGAC 26280
TGGATTGATG GAGAAAATTT TCGCAAAATA CCAATAGGAG CTTTATTTCT GAAACTACTT 26340
TCAAAGGCTC CAAACGCTAT TCTATAAGCG AGAAACTAAA ATCGG 26385

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2716 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CCTGCCCGCA TTGCCCTAGG CATTAAGTAA ACATATAAAA GCATGTGAGA GACTGTTGGA 60

AAAGCGAGGA AATTTCCCCT CTTTTCCTCT AGTCTCTCCT TTCTTTTGCT GATTTTATTC 120

AAAGAAAATG ATATAATAGT AGTTATGGAG AAAAAGAAAT TACGCATCAA TATGTTGAGT 180

TCAAGTGAGA AAGTAGCAGG ACAGGGAGTT TCAGGTGCTT ACCGTGAATT AGTTCGTCTT 240

CTTCACCGTG CTGCCAAGGA CCAATTGATT GTTACAGAAA ATCTTCCAAT CGAGGCAGAT 300

GTGACTCACT TTCATACGAT TGATTTTCCC TATTATTTAT CAACCTTCCA AAAGAAACGC 360

TCAGGGAGAA AGATTGGCTA TGTGCATTTC TTGCCAGCTA CACTTGAGGG AAGTTTGAAA 420

ATTCCATTTT TCTTAAAGGG AATTGTGAAA CGCTATGTAT TTTCTTTTTA CAACCGGATG 480

GAGCACTTGG TTGTGGTCAA TCCTATGTTT ATTGAGGATT TGGTAGCAGC TGGTATTCCA 540

CGTGAAAAAG TGACCTATAT TCCTAACTTT GTCAACAAGG AAAAATGGCA TCCTCTACCA 600

CAAGAAGAGG TAGTCAGACT GCGCACAGAT CTTGGTCTTA GTGACAATCA GTTTATCGTA 660

GTAGGTGCTG GGCAAGTTCA GAAACGTAAA GGGATTGATG ACTTTATCCG TCTGGCTGAG 720

GAATTGCCTC AGATTACCTT TATCTGGGCT GGTGGCTTCT CTTTTGGTGG TATGACAGAT 780

GGTTATGAAC ACTATAAGAA AATTATGGAA AATCCCCCTA AAAATTTGAT TTTTCCAGGC 840

ATTGTATCGC CAGAGCGGAT GCGCGAATTG TATGCTCTAG CGGATCTTTT CTTGTTGCCT 900

AGTTACAATG AGCTCTTTCC TATGACTATT TTAGAAGCTG CGAGTTGTGA GGCTCCTATT 960

ATGTTGCGTG ATTTAGATCT CTATAAGGTG ATTTTGGAGG GAAATTATCG GGCGACAGCG 1020

GGTAGAGAAG AGATGAAAGA GGCTATTTTG GAATATCAAG CAAATCCTGC TGTCTTAAAA 1080

GATCTCAAAG AAAAGGCTAA GAATATTTCC AGAGAGTATT CTGAAGAGCA TCTGTTACAA 1140

ATCTGGTTGG ACTTTTATGA GAAACAAGCC GCTTTAGGGA GAAAGTAAAA AGTGAGGTAA 1200

TCTATGCGAA TTGGTTTATT TACAGATACC TATTTTCCTC AGGTTTCTGG TGTTGCGACC 1260

AGTATTCGAA CCTTGAAAAC AGAACTTGAA AAGCAGGGAC ATGCTGTTTT TATCTTTACG 1320

ACGACAGATA AGGATGTCAA TCGCTACGAA GATTGGCAAA TTATCCGCAT TCCAAGTGTT 1380

CCTTTCTTTG CTTTTAAGGA TCGTCGCTTT GCCTACCGAG GTTTTAGCAA GGCACTTGAA 1440

ATTGCTAAAC AGTATCAGCT AGATATTATC CATACTCAGA CAGAATTTTC TCTTGGCCTG 1500

TTGGGGATTT GGATTGCGCG TGAATTGAAA ATTCCAGTCA TCCATACCTA TCACACCCAG 1560

TATGAAGACT ATGTCCATTA TATTGCTAAG GGGATGTTGA TCCGGCCGAG TATGGTCAAG 1620

TATCTGGTTA GAGGTTTCCT GCATGATGTG GATGGGGTTA TTTGCCCTAG TGAGATTGTC 1680

CGTGACTTGC TATCTGATTA TAAGGTCAAG GTTGAAAAAC GGGTCATTCC TACTGGGATT 1740

GAATTAGCCA AGTTTGAGCG TCCGGAAATC AAGCAGGAAA ATTTGAAAGA ACTGCGTAGT 1800

AAACTAGGGA TTCAAGATGG TGAAAAGACG TTGCTTAGTC TTTCGAGAAT CTCCTATGAA 1860

AAAAATATTC AAGCAGTTTT AGCAGCCTTT GCTGATGTTC TGAAAGAGGA AGACAAGGTT 1920

AAACTGGTAG TAGCTGGGGA TGGCCCTTAT CTGAATGACC TCAAAGAGCA AGCCCAGAAC 1980

CTAGAGATTC AAGACTCAGT CATCTTTACA GGGATGATTG CTCCTAGTGA GACGGCTCTT 2040

TACTATAAAG CGGCGGATTT CTTCATTTCG GCATCGACAA GCGAAACGCA AGGTTTGACC 2100

TACTTGGAAA GCTTAGCCAG TGGAACACCT GTCATTGCTC ACGGAAATCC TTATTTGAAC 2160

AACCTCATCA GTGATAAAAT GTTTGGAACC TTGTACTATG GAGAACATGA TTTGGCTGGT 2220

GCTATTTTGG AAGCCCTGAT TGCAACACCA GACATGAACG AGCATACCTT ATCAGAGAAA 2280

TTGTATGAGA TTTCAGCTGA GAACTTTGGG AAACGAGTGC ATGAGTTTTA TCTGGATGCC 2340

ATTATTTCAA ATAACTTCCA GAAAGATTTG GCTAAAGATG ATACGGTCAG TCAGCGTATC 2400

TTTAAGACAG TTTTGTATCT TCAGCAACAG GTGGTTGCTG TACCTGTAAA AGGATCTAGA 2460

CGCATGTTGA AGGCTTCAAA AACACAGTTG ATCAGTATGA GAGACTATTG GAAAGACCAT 2520

GAAGAATAGA AAGAGGAACA GCTATGAAAA AAACAATTAA TGAGAAGCGG TCGTGATAAA 2580

AAGATTGCGG GTGTTTGTGC TGGGGTGGCC CATTATCTGG ATATGGATCC GACTATCGTT 2640

CAAGTCATTT GGGGTGTTCT TACTTGCTGT TACGGAGCTG GAATTGTAGC TTACATTATT 2700

TTATGGATTA TCGCGA 2716

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13926 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTTTGGTTTT GCCTTATTCA AGACATGAGG GCCATCAGGA ATGATCTGAA ACTGCGAATC 60

```
TGTTAACAGT CTATGGAGAG CTTTCATAGA ACTAAGATTC GGTTTATCTT TGCTGCCACA    120
AATTAGTAAG GTTGGATAAG GGTAAGTTCC TGCTATATCC GTTAAATCAA GTGTCTTCAA    180
CTCCTCAGAA ACTCCGACCA TAAGAGTCTT GTCTGCTCCC TGTTTTTCAA ATACTCTTTT    240
GGGAAGTAGT TTAAAAATCA GCAATTGAAG ATAAAATAGG ATATTCCCTG CTAATTTAAG    300
CGGGCATCCT GACAGAATCA AAGCTCGAAG ATTTGGTAAA TCGTAACTGG AAAGTTCTAG    360
TGTCAGGGCA GCACCTAAGG ACAATCCAAT CAAAACAAAA GGTTCTGTCT CTTGAGCTAG    420
GTGCTGATAA ACTCGCTCTT TAGCTTGTTG ATAGTTACTA ACTCCAGAAG GAAATAACTC    480
GATAGCCTCA GAAGGATAAT CTGTCAGTAG ATTCCGAACT TCTTTCCAAG ACTCTGCTGA    540
CTGCCCTAAC CCATGCAAAA ATATTAATTT CATCTAGTTC TCCTCAAGGC TTAATTCATA    600
CAAGCCTCTC ACTGCATTAC AGCCGTAAAT AGCTTCTGCT TGGGTTAAAT CTGCCAAGGT    660
CAAGACTTTC TCTTCTACCT GTCCTGTTTC TAGCAAATGC TGACGGTAAA TTCCTGGCAA    720
GATTCCAAGT CGGATAGGCG GTGTGTAGAG TTTTCCAGCG ATTTTCAGAA CCAAATTTCC    780
TATAGAGGTT TCAAGCAGTT CTCCTGACTT ATTGTGGTAA ATCTTCTCTT GTTCTCCTAG    840
GCTCAAATGC GGTCGGTGAG TGGTTTTAAA GTAGGTAAAG GATTGATTCA AAGCAGCTTC    900
CTGAAGACAG ACTTGGGCCT GACAAAAGCT TGTACTGAGA GGGGTTAATA CTTGACGATT    960
GACTTCTATC TCTCCAGATT TGCTAAGGCT GATTCGCAAG CGGTAATCTC GATTAGCTTC   1020
ACAATCCTGA CACTCTTCCT CAATCTTGTG TCCCAAGTCT TCTGCATCAA AAGGAAAAGC   1080
AAAATAACGA CTAGCTTTTC TCAGCCTTTC CAGATGTTGT TCTTCAAACA TCAGTTGTTT   1140
TTGGCTGATT TTTCCAGTTG TAATTAATTG GAAGCGAGCT TGTTTACGAT AGAGAACTGC   1200
TGCCTTTTGA TGAACCTCTC GGTATTCAGA TTCCCATGTG CTATCCCAAG TAATCCCTCC   1260
GCCAACTCCA TAAATGGCTT GACCTTTGTG AAGTTGAATG GTACGAATGG CCACATTAAA   1320
AATCCGTCGT CCATTTGGAA GCAAGAGACC AATCGTTCCA CAGTAGACTC CACGCGGTTG   1380
AGGCTCCAAG TCCTTGATAA TCTCCATTGT CGCAATTTTC GGTGCACCCG TTATGGAACC   1440
ACAAGGAAAG AGTGAGCGGA AGATTTCAAC AAGGTCCACA TCCTCTCGCA ACTGACTCTT   1500
GATGGTCGAA GTCATCTGCC AAACAGTTGA ATACTGCTCT ACCTGACACA GACGCTCCAC   1560
GTGCTCGCTC CCAACTTCAG AAATACGGTT CATATCATTG CGCAAGAGGT CCACAATCAT   1620
CATATTTTCA GAGCGATTTT TGGGATCCTG TTCCAACCAA CTGGCCTGTT CAAGATCTTC   1680
TTGGTCAGTT ACCCCACGCT GAGTCGTCCC CTTCATTGGT CGTGTTGTCA ACTCGCGATC   1740
ATTTTGCTCA AAAAAGAGCT CTGGGCTCAT GGAAATCACT GTCATCTCGT CATGTTCCAC   1800
```

ATAGGCATTG TAGCCCGCCT CCTGCTCTAC CACCATACGA TTGTAGATGG CAAAAGGATT 1860

GGCATTTAAC TTTTGCTTAA GTTGGACGGT GTAGTTGACC TGATAGGTAT CTCCCTGCCG 1920

TAAATGATGG TGAATTTGGG CAATGGCCTT TTCATAGTCT GCTGCAGACG TTACTTCCTG 1980

CCAATTTGAG GGCAAATCAA TATCCTCATA AGTCAGAGGA ATAGGGGAAG TTTCTACGAT 2040

ATCATGAACA GTAAAGTAAA GCAGGTACTC TCCCAGTAGG GGATCCTTGT GAACTGCTAA 2100

TTTTTCCTCA AAAGCAGGTG CAGCCTCGTA GCTGACATAC CCCACCACAT AATAACCTTG 2160

CTCTTGGTAG CTTTCCACTT GTGCCAGCAA ATCTGCCACT TCTTCTACAT TTCTCGTTTT 2220

CAACTCTTTA ATAGGCTGGG TAAAGGTATA TCTCTCCCCC AAAGTCCTAA AATCAATCAC 2280

TGTTTTTCTA TGCATACCTT AAGTATAGCA TAAAATAAGA AAACCCTCAT CCGCAAAGCA 2340

GATGAGAGAT TTCAATTATT TAAAGATTGA AGTTTTAAAG CTATTTGTTT GTTGAAGAAG 2400

TTTCTTATAA ACAGCTTCTT TTAATTTAAC TGTATTATTC ATAGATACTG TTTTATTACC 2460

GTTTGCTTCT TGTTTAAGAG TTTCGGCATC TTTTTTAACA GCTTCTTTAA ACAATGTCAG 2520

TAAATCATCG TATGATGAAA CGGAAGAACC ATTTACTTCG AATGTTGTTA ATCCTTTCGT 2580

TGCTTTATCT TTAACTTCTT TGAAGTAAGC TTTTTTAAAT TCTTCAATAG TATTAAATGT 2640

ATTGTTAGAT ATTTTCTTGA TAATATATTC ATCACTTAGA ACAGACTCAC CATCTGTTTT 2700

AGATTGTTGT TTATATTTAT TTGAAGCATA ACCTAAGAAC CCATTTTCGT ATCCGTAGTA 2760

ACCCCATAAT CTAAAAGCAT TATGTTTGAA TGAAACAGCT CCAGGAGCAC CTTTACTAGT 2820

ATTACCTCCG TAGATACCGG TCATCATTCT AACACCTACA TAAGGTGATT GATCGTTATA 2880

GCTAATTGCT TCGGGTTTAT AGATACCATT ACCTGGATTG CGATTAGTCA TTAATTGTTG 2940

ATCAACTAAA TCATTAACAG ATTGAATATT TAATTCATTT TTCTCTTCTT GACTTAGATT 3000

TCGAATTTTA TCCCATTGAT TTAATTTATT GTTATCACGG TATTCTCTAT CTATTTTTTT 3060

GAACCATGCA CTATTTAAAT CTTTATTTTG TTGAGAAATC ACAGATTCAG CCTCAATTTC 3120

ATCAAGAAGA GTTAAAGTGT CATTATAACC CTTCATATAT CTATTAATAT CTTCTCGTGT 3180

TTTTAGAGTT TTTGGATCTG TAATATACCA CTGATTCCCA TCATTTTTGC GTTTAAATAC 3240

CATATTAATA CCTAAAGAAC CAAACTCATC AAATCCACTA CCAGTAACAG GAGTTTGTAG 3300

CATACCCTGA GCATATGCTT CAGCATCAGT ACCTTCACGG TGTCCAAAGC CACCTAAGTA 3360

AATCGCACGG TCGTTGACGT GTGTTGTTTC ATGTGTGTAA ACTGAAATAC CGTATTCACC 3420

AACCATTTCT AAATGAACAT ATTTTACATC AGTTCTAATA TCATCAGAGT TAGGATATAT 3480

AGCAGCATAA GCTCCTGTTC CATTATAATT ATAATACTTA TCCATAGGAC CAAAGAATTC 3540

TCTAAGAGGA GTATATACTT TGTCGGTATT ATAGCGGCCA TATTTTTCAA CCCATCCACC 3600

AGGAGCGTTA TAACCTTCCC AAATAGGAAT AACAGCATCT CTTAGTAGTC GTTGTTTAAC 3660

GTTATCAGAC GCTAGACGAT ACCAGAAATC ATAATAGTTT CTATAACCAT CTGCAGCTTT 3720

GTTAACGATA TCTTTAATAT CTTCTAATGA TTTTTTACCT AATCGCTCTG CACTACCAAA 3780

GGCAATTGCA TTATAATTTG AAATTAAATA AAGATGTGCT TTATCAATAT TCAGTAGTGG 3840

GAGTATAGTA TTTCTAAGGT GACTTCGTTT TAAATTATCG AATGCACGAT GTTTAGAATT 3900

TTTAATTTCT TCGACCTCAG AAGCGCGTTC TGCGATGTAG ACATGGTCTT CTGTAGCATC 3960

AATAAACCAA TCGTTCATAT TGTCTATATT TGTGAACAAT TGTCTATTAT AATTTAAAAA 4020

TGCATCTAAA TTACCTGATT TAGTATATTT AGCCAATACT TGACCGAATG CGTCGAATGT 4080

ACGTGAACCT TTAATGTTGT TCTCTTTAGA ACCGATTTCA ATTAATCTGT CTAATACGCT 4140

AACTTTTTCA CCATAGAAAT CTGGTTTGAA TAGCATTAAT TCTTTAATAT TAACATCACC 4200

AAATTTAACT CCATAGTAAC GATTTAGGTA AGTTAAACCT AGTAATAAAG CTGCTTTGTT 4260

TTTCTCGACT TTATCACGAA TCATTTGACG AGCAGCTGGA GAATCATTTA GTTGATGTTC 4320

TTCGTTTTGA ACTAATTTTG TGATTAGGTT TGTTAAGTTT TCTTTAACAT CTGTGAAGCT 4380

TTCTTCTAAA TATAAATCTT TGATTGCATT AACTCTATAG TCACCTAATC GATTTAGATG 4440

CTGATACATC GTTTGAGACT GAAGCTCTAC TGATTCTAAA ATAGATTTTA TATCATTAAC 4500

AAGAGTAGTG TTATCTTTTT GAACGATATT AGGTGTATAT TTAATTCCTA AGTCAGTTAT 4560

AGTATATTCT TTTACATTAC TTAAACCTTC ACTGCTAGAA GACAAGTTAA AGTAATCTTT 4620

TGTACCGTCC GCATAGTGAA CAATAATTTT ATTAGCTTCA TCTAGGTTTG TGATAAACTC 4680

ATTGTTGTTC ATCGCGGTAA CAGAAAGAAC TTCTTTAGTA TTTAGATGGT GTTCTTTATT 4740

TAATTTATTA CCTTGATATA CAATATAATC TTTATTGTAG AATGGTATTA ATTTTTCAAG 4800

ATTTTTATAG GCTTGGTTAT ATTCAGCGTT ATAATCTTGA ATACTAGAAT AGGCTTTTTC 4860

TTCATTAAGT TTTGCAAGAG GAGATAGATC ACTTTCTAAT TTATCAGCAG TAATATTGAA 4920

AGTAGTAACT TTAGCATCAG CTTGTTCTTT AGTTAATTTA GTAAATGTTT TAGATTTCCT 4980

AAATGATCTA TTACCTGACG AATATCCCTC TACCGCATAT AAATCTTTTA TATGAGCACT 5040

AGCATAATCA GAATCATCAA CGTCGTTAGA GCCGAATAAC TCCTCTCCAC GGATAATCTT 5100

AGCATAGCTG ACAGAATTAC TTACCGTACC TACAGGCCAA GTCTTACTTG CTATTGCTCC 5160

AACTTCTACT GGATTTGAAA CATCTATTTT ACCTTTTACA ACCGACTCAG TTAGGAGAGC 5220

TTTTGTACCA ATAAGATGGT CTAGAGTTAA TCCATAATCT ACTTTAGGAA CTAACAAGCT 5280

GGCGCGTGTT TTGTTTCCTG TAATAGTAGC ATCAACATAT GCTTTTCTAA CAATTCCTCT 5340

ATAGTTTGTA CCTGCAATTC CCCCTGTATG AGAGCCATTT CCACTTGTAG AGTGTAGTTT 5400

GCCAAAGAAA GCAACATTTT CAATACGAGT TCCATCATTC ATATTATTTA CAAATCCAGC 5460

AACATTATTA CGACCTGAAA GTGTGCCTGT AATTTTGACA TTTGTAATAA CTGAAGAACC 5520

TTTCATAGTA TTGGCTAATG ATGCAATATT ATCTTGACCA GAACGTTCTA TCTCTACATT 5580

TTCAAAATTC ACATTATTTA TCGTTGCGTT TGTTATCACA TTAAATAATG GATGTTCCAA 5640

TTCAGTAATA GCAAATTGTT TTCCTTCAGA ACTTAAAAGT TTTCCTGTGA ATTCTTTAGT 5700

GATATATGAT TTTCCATTAG GAACAACATT TCTAGCGCTC ATTGATTGTC CCAGACGATA 5760

TTCTTTTGAA GGATCGTTTT GAATAGCTTC CACTAATTCT TTGAAATTAT AATATACATT 5820

ATCTTCGTGG ACTTTAGGTT TTTCAATATA GTGAACGTAT TCTTCTTCAA ATTTATTATC 5880

AGCAGTTCTA GAGACTAAAT TGTCTGCGAT TGCTGTAACT TTATATACAG GTGTTCCGTT 5940

AACCGTAGTT TCTTCTATAT TTTTAACAGC TAGTAATGTA GTTTTCTGAT TATTTGAAGT 6000

TATTTTTAAA TAATAATTGC TCTTATCATC AGGAATAGTT GTTATCAGTG ATTCATTAGT 6060

TTCTTTTCCA TTTTCGTATT TGATTAAATC TGTACGTTTA ATATTTTTAA GCTCAACTTT 6120

TTTAAGATCT AATTGAATAT TTTGATTTTC TAGAGTTTCA GTTTCTTCAC CGTTACCTCT 6180

GTCGTAAATC ATAGTTGTAG ATAGGGTGTA TTCTTTGTAG TACTCTAGGT TCTTAAATGC 6240

AGCGCTTATA GTTTCTGTTG TTACCTTGTC ATCTGTAAGG ACTACAGTAT TAATAACTTC 6300

TTCTCCTTTT TTCAATTCAG CTGTGATTGA TTTGATTTTT GTTTTGTTTT GATTTTCTAG 6360

AGTATACTTA GCAACAGCTT CACGTTCCAA TATTTTCTTA TCGGTACTAG TCAATGTTAA 6420

TATTGGCTTT TCAGATAATT CAACCAATTT TTCAATAGTT GCAGTTAATT TTTCAACAGC 6480

TTCGTTAACT TCACTTTGTT TAGCATCTGT ATTAGCTGCA ACTTTTTCAG CCTTTGTAAC 6540

TTCAGTTTGG AGGTTTTGCC AACTTCTATC ACTGTAATGT TCTTTTACCT TTGTTTTTGC 6600

ATCTGCAATC GTATTGTTTA ATTCAGTTTT ATCAACGTTT AGAGCGTCAA TAGCCGTTTT 6660

AAGTTTATTT GTCTCGCTAT TTACCTCAGG CTGTTTTACA GGCTCTGAAG CATAGACACC 6720

TTTTGCAGTT TCTAAAACAG GTCCAAGAGC ATTGTAACTT GCTGTAGAAT AATCAGTAGG 6780

AGAAACTGAA CTAGCTTTAT CAATTTGATT ATTTAACTCA CTTTTATCAA CTGGTTCTTT 6840

AGTACCAATA CCCTTTATTT TATCTTCTGG TTTCGGTGTT TCCTCTACAG CCTTCTCTTC 6900

TTCAGGAACT TCTGGTTGCT TTTCTGGCTC AACTGGTGCC GTTGGTGCCT GTTCGTCTTC 6960

TCTTGGCGCG ACTGGTTCAC CTGCTTGTTC AACTTTTGGT TCCTCTGTTG GTTCTGTTTG 7020

TTTTTCTACA GCAGGCGTTT CAACTTTTGG TTGTTCAATA GATTGATTAA CAGTCTCCTC 7080

TTTTGGTTCT ACAGTTTCTT CAGCCTTGGT ATCTGGAGTT GACTCTTCTT GTTTCGGTGT 7140

TTCCTCTACA GCCTTCTCTT CTTCAGGAGC TTCTGGTTGC TTTTCTGGCT CGACTGGTGC 7200
CTTTTCGTCT TCTCTTGGCG CGACTGGTTC ACCTGCTTGT TCAACTTTTG ATTCCTCAGC 7260
TGGTTTGTCT GATGGTTGAC TTTCTGGCTT AACTGCTACT TTTTCCTCTG GTTTTGACTC 7320
AACTTCTCCA CCTACTTCTT CAACTGGAGC TGGTTCTGCT GAATCTTCTT TCCCCTCTTC 7380
TACTTTAGGA AGGGTGTCGT CAGTAGGTTT TACCTCCGAT TTTGGTTCTT CCTTTGGACT 7440
TTCTTCTGTT TTAGGTGCTT CTTCTTTTGG AGCTTCCTCT GTCTCTACTA CTTGGTTTTC 7500
TGTCCTAGCT TGCTCCTGAT TTGTTATTGA TTGAGGAGTC TCAACTTCGA CCACAGTCAC 7560
CTCTCCAGGT TTTGCTGAGG TTTCTTCTAA AACAGTGTCC AAGCCAAGCG TTTTGAGGAT 7620
GTCACCTGAT AGATAACCAA CATAGCGATA GCCCTCCATT TCAACAACAC CCTCTCGACT 7680
AGCCAGCGCT AGGGTCGCAA CTGGGTCTAC AGCCCCTGCA CTAGGAAGAA CTACCAATCC 7740
CATAGCTCCA ACTAGAAAGA CGCTAGCAAT TTTCTTTCTC TTGTAGATTA AAAGCAAGCT 7800
CCCAACAGTC AGCAAACCAA AAGCTGTCAA AACAGATGCT TCTGTCCCTG TTTGAGGCAA 7860
CTGATCTTTT TGATACACCA AACCATATAC AACTTCATTC CTGTCAGGCT TTCCTGTCTG 7920
AATTAAATCT TTAGCTTCTT GTGAAATAAT CTCTTTATTT ACATAGTGAT AGGTGGCTGC 7980
GTCCACTACA GAAGGAGCCA TCAAAAGGCT TCCAAGAAAT ACAGAGCCTA CAACTCCCTT 8040
AATCTTACGA ATTGAAAAAC GGTCTTTTTT AAACACTTTT ATCTCCTTTA TTCATTCTCA 8100
AAACTTCCTA ATAGCATCTT GCGGATAGTG CGCACGCGCA CCTCCGATTA ATTTTGGACG 8160
ACTAGCCAGT GCCGTTACAT GGGCATGACC AATCTCTCTC AAAATAGGGC GAATCGGAAC 8220
CTGAACATGC TTGACATGCA TGCCAATTGC AGTGTCTCCG ATATCCAATC CAGCATGAGC 8280
CTTGATAAAT TCAACCTCAA CTGGATCCTG CATAAACTTA AAGGCTGCCA ACTGCCCCGA 8340
ACCTCCTGCA TGAAGAGTAG GATGGACACT GACAATTTCC AGACCAAACT GCTCTGCCAC 8400
CTGACGTTCA ACAACGAGAG CCCGATTGAC ATGCTCACAA CCTTGAACTG CTAAATGGAT 8460
ACCTCTACTA CCTAGAATAT CCAAGATAGT CTCCACTATC AGCTCACCAA TCTCTTGACT 8520
GGATTCTTTC CCAATATGAC CACCTAGCAC CTCACTAGAA GATAGACCTA AAACAAAAAG 8580
GGCCCCCTGC TTCAAATTGG TCTTTTCTAA AACATCTTCC ACTACCTGAC GTGTTTCTCT 8640
TTGAATCTGT GTCTCGTTCA TCTCTGTTAC CTCTGTTGTC ACTCTTCTAT CATACCGTTT 8700
TTTCTTGTTT TTAGCAAGAT AGACAACCTA GAAAGTTTGC CCAATTACGC ATAAAACTCC 8760
CAGAATTGAC TGGGAGTTAG CTAGTTTCTA TTCTATTTAT ATATATTTCA ACTTTCGTCC 8820
CTTTTTGGGG TCTAGAATCA ATCTTCATAT GGTAATTGGC TCCAAAATGA AGTTTGAGCC 8880

GTTGATCGAC ATTTTGAAGA CCAACTCCCC CACGTTTGAG TTGACTTTGA CTACTATCAC 8940

CAGCATCTTG GAAGCCAACG CCATCATCCT CAATACGGAT GACCAATCCC GAATCCTGTT 9000

TCTGGACAGA AAGTTTAATA TGGCCCTGAC CTTCCTTTTC CTTAATGCCA TGGTAAAGAG 9060

CATTTTCTAC AAGGGGTTGT AGGACCAGCT TGGGTAAGAC TAAATTATCA AAGGCAACAT 9120

TTTCATTAAT TTCGTATTCC AGCTTATCTC CATAGCGTTG TTTCTGGATA AAGAGATACT 9180

GGCGGACATG ATTGATTTCG TCAGAGAGAC AAATCAAGTC CTTGCCTTGA TTGAGCGCCA 9240

AGCGGAAATA GGTTGCCAAG GACTTGGTCA CCTGCACCAC TCGCTGACTA TCATGAAATT 9300

CAGCCATCCA GATGATGGTG TCCAAAGTGT TATAGAGGAA ATGTGGATTA ATCTGGCTCG 9360

AAAGGGCTTG AAGTTGGTAC TGACGGGTCG TTTCTTCCTG GCTACGAATA GCTACCATCA 9420

ACTGATCAAT CTGATCCAAC ATAGCATTAA ATTGGCGAGT TACTTCTCTC AGTTCATAGG 9480

CACCAACTTC CTTGGCACGA AGATTTTGAG CACCAGAAGC AATTTCCAAC ATGGTTTCTC 9540

TCAAATCCTT CAAAGGAGCA ATCCAGCGTT TAAGACTGAA CCACACTAAG CAGAGACAGA 9600

CAAGAAGAGA TGTGACACTG GCCCCAAGCA AGGTCCACAA GAGCTGACTC CGAACCTGGT 9660

CTAACTTTTC CAATGATGAC ACGCCAAGCA CCGTCCAATC AGTTCCTGCA ATCTTCTCTT 9720

GACTGACGTA GGATTTGTGA CCAGGAGTAT AACCCTGACC TGTATCGATG TAGGGTTTCA 9780

TAGCCTCCAT TTTGCTAGAC GAACTATAAA CTGTGTGTTG AGGATGGTAG ACAAATTCAT 9840

GGTTTTCATT GATAATGAAG GCAAAGCCCT GCTGCCCCAA CTGGAGTTGA TTGAGATAGG 9900

CTTCCAGAGT TTCATAAGAA ATATCCAAAC GAAGCACACC AAGATTGGCT CCCTTTGCAT 9960

CAACAAGTTC TTGAGTGACA GAAATGACCC ACTGACTATC TGATTTACGA GCTGGAGTCA 10020

AAACAGGCAT AGCTCCCTGA TGAATGGCCT TTTGGTACCA ATCCTCAGCC ATCATATCAG 10080

AGGAAGTTTT CATCTGCACA CTGTCATCTG TAGAAATGAC CTGACCAGAT TTGGTCACCA 10140

GCACAACAGT TTTCAAGTCC TTATCTGACT TCAAGATGGT CAAAAACAAA TCTCGGATTC 10200

CCTCGACCTT GTCTTGACTG GGATTCTCAG CATAGGCCAG AACATCCGTC TGCTGGGTCA 10260

AACCAGTCGA GGTGGTTTCT AGTTTTTTGA TATAAGACTG AATAAAGTGG CTAGTCTGGC 10320

TGATGGTCGT TTGGCTGTTG CCCTCAATGG TGGCCTCAAT GGCTGAAGAA CTTGATTGAT 10380

AGTAGAAAGT TCCAACCAGA GCTAGGAGAA TGAGAAAGAC CAGAAAGATG GAAATAACCA 10440

TTCTAACTAA AAGAGAAGAA CGCTTCATCG GTCTTCTCCC TTCTTAAACT GACGAGGTGT 10500

CACACCTGCA ATCTGCTTAA AACGTTGGGT AAAATAGTTC ATATCTTCAA AACCAACCTT 10560

CTCTGCGATC TCATAAATCT TCAGATCTGT AGTTAAAAGC AAGAGCTTGG CTTGTTTAAC 10620

ACGTTCTCTC ACCAGATAAT CCTGAAAAGG CAAGCCCAAC TCTTTCTTAA TCAAGGAACT 10680

CAGATAGGTC GGACTAAAAC CTAAGTCACT GGCTAAAGAC TTTAAACTAA ATTGGCTATC 10740

AGCCAGATGA GACTGGATTT TCTGGGCCAT GTTTCCTTCA AACCTATTAG TCAATAAATC 10800

TTGTAACTGC TCTTCTTTCT CTTCCTTGTC TAGTTTTTGT TTGATTTTCC CCAACATTTC 10860

CTCAATATCC TGACGAGAAA AGGGTTTGAG CAGGTAGTCG TCCACACCTA GTTTGACAGC 10920

AGACAAGGCA TAATCAAAAT CATCGTAACC TGTTAAAAAG ACCAAATGAA CCTGAGGATA 10980

GGTTTCTCGT ACCAGACTGG CCAACTGGAT GCCATTTAGA TGAGGCATGT TGATATCGGT 11040

TAAAATGATA TCTGGCACCT GCTTTTGGAT CAATTCCCAA GCCTGCCTTC CATTTTCAGC 11100

CTGACCGATG ATTTCCATAT CGTAGGCTGC TACATTGACC AGTTTAGTCA AACCTTGTCT 11160

TACCAGATAT TCATCTTCTA CGATTAAGAT TGTGTAGGTC ATGCTCTGCT CCTTTACCAC 11220

TTACTAGTAT CAGTATAGCA AAATTCTCCT CTAACTGCTT AGGAAAGACC TCTTATACTC 11280

AATAAAAATC AAAAAGTAAA CTAGGAAGAT AGCCACAGGT TTCTCAAAGT ACCGCTTTGA 11340

GGTTGTAAAT AAAACTGACG AAGTCGACTC AAAGTATAGC TTTGAGGTTG TAGATAAAAC 11400

TGACGAAGTC GATAACCCTA CATACGGTAA GGCGACGCTG ACGTGGTTTG AAGAGATTTT 11460

CGAAGAGTAT TAATCAACAT AATCTAGTAA ATAAGCGTAc CTTTTTCTTC CATTTGGTCT 11520

TTGGGAATAA AGCGGATAGA GAGGCTATTG ATACAGTAAC GTAAGCCGCC CTTGTCCTGT 11580

GGACCATCCG TAAAGACATG CCCAAGGTGA GAATCTCCTA CTCGGCTCCG CACTTCCATA 11640

CGCGTCATAT TGTAGGACTT ATCTTCCTTG TAGGTGACAA CATCTGGACT GATGGGTTGG 11700

GTAAAACTAG GCCAGCCACA ACCAGACTCA AATTTGTCTT TTGATGAAAA GAGAGGTTCC 11760

CCAGTTGCTA TATCCACATA GATACCGGAT TCAAATTTAT CCCAGTAACG GTTTGAGAAA 11820

GCTCGTTCTG TTTGATTTTC CTGGGTAACT GCATACTCCT CAGGTGACAG GGTCTTTTTC 11880

AATTCCTCAT CACTTGGTTT TGGATATTTG CTGGCATCAA TGACAGGATA GGCCGCCTGA 11940

TTAACATTGA TATGGCAGTA GCCATTTGGA TTTTTCTTGA GATAGTCTTG ATGGTAATCC 12000

TCAGCCACCA CAAAATTCTT CAAGTTTTCC TTTTCAACTG CTAGAGGTTG ATCGTATTTC 12060

TTAGCCACCT CATCAAAGAC TTGGTTAATC ACTTCCAAAT CCTTGTCATC TGTGTAATAA 12120

ACACCAGTAC GGTACTGGGT CCCCACATCA TTTCCTTGTT TATTTTTGCT GGTTGGATTG 12180

ATAATGCGGA AATAGTGAAG CAGGATTTCC TTGAGAGAAA TTTGCTTGGC ATCATAGGTG 12240

ACATGGACGG TTTCTGCATG ACCTGTTTGG TTAATCAATT CGTACTTGGT TGTTTCTCCT 12300

CTACCATTTG CATAGCCTGA AACGGCATCC GTCACCCCGG GAACACGTGA GAAATATTCC 12360

TCCACTCCCC AGAAACAACC TCCAGCTAGA TAAATTTCGT GCAAGTCTGC GTCTTTACTA 12420

ATTTCTGTTT TTTTCACTGC TTTTCCTCCT TGGCTAACTG CCGCCTTTTC AATTTGCGAG 12480

GCATCTGTCT GCCCTGCATT TCGTATCAAT AGAACATAGA AACCGGTTAT GGCTAGAAAA 12540

AATACTCCTA GCAACAAGAA GATTTTTAAC TTATCATTCA TAAGACGCCT CCTAGGCTAA 12600

TTCCTTCAAA GTTTGCAAAA TTGCATCTTT TTCCATGAAT CCTGGATGTG TTTTGACCAG 12660

CTTGCCTTCT TTGTCTATAA AGGCTTGGGT TGGGTAAGAA CGGACACCAT AAGTTTCCAA 12720

AAGTTTGCCT GATGGGTCAA CTAGGACTGG GAGATTTTTA TAATCCAATC CCTTATACCA 12780

ATTCTTAAAG TCCGCTTCAG ATTGCTCTCC CTTATGTCCT GGTGACACTA CTGTCAAGAC 12840

CACATAGTCA TCACCAGCTT CTTTAGCAAT CTCATCCGTA TCTGGAAGAC TAGCCAGACA 12900

GATGGAACAC CAAGAAGCCC AGAATTTGAG ATAGACTTTC TTGCCCTTGT AATCAGATAA 12960

ACGGTAGGTC TTGCCATCTA CTCCCATCAA TTCAAAATCA GCCACCTCTT TCCCTTTAGC 13020

TGCGCTTGTT TTACTAGCTG TCTGCTCCGT CTTCATTTCA TCTTTCGTTT GGTGTTCACT 13080

AGTCACGGAC TTGCCTGAAC AAGCCGTCAA ACAAAGGAGC GAACCTGCTC CAAGAACACA 13140

TGTTTGCCAT TTTTTCATAT TGATATTCCT TTCCATTTTA TTCAAATAAT TGACTTAAAA 13200

TTGAAGCATT TCCAAACAGA ACCAAGAAGC CCATCACAAT AATGAGAAAA CCACCCACTT 13260

TTTTGAGGAT TCCGAGATAG GGATGAAGTT TTCGGAAATG TTTCAAAACA TAACTAGAGG 13320

TCAGAGCTAG AAGCAAGAAT GGTAGCGCCA AGCCCAGCGT ATACACCAAC ATGAGACCAG 13380

CTCCCTGCCA AGCTCCTGAA CCACCTGAAG CCGCCAAGGC CAAAACAGAC CCCAGAACCG 13440

GCCCCACGCA AGGCGTCCAA GCAAAACTAA AGGTCAAGCC CAATAAAAAT GCCTGACTAT 13500

AGCCCTTACC ATTTTGCCCC TGTCCTTGCA GTTGTAGCCT CTTTTCCTTA TAAAGCCCCT 13560

TAAAGTGTAG AATCTCCATT TGGTGCAAAC CAAGAAGGAT AATAATTGCC CCAGTAAGAT 13620

ATTGGAACCA AGAAGCATAA AGCAAATCGC CTAAAAAACC AGCTCCATAG CCCAACAAAA 13680

TAAATATAAA GGAAATTCCT GCTATAAAGG CCAGAGTTCG TAATAAACTA GTAACTGAGA 13740

TTGAAAATTT GCCGCTAGAA GCCTGAGCAC CATCCTTATC ATCTAGTAAC ACTCCTGTAT 13800

AGACCGGTAA CAAAGGTAAG ATACAAGGAG AAAAGAAGGA TAGAATCCCT GCCAAAAAGA 13860

CACTTAGAAA AAAGAAAATA TGACCCATAA AGTTCCTCCT ATCATTTTAT TGATAGATTT 13920

ATTATA 13926

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CCCAGCAGAA AAATGGCATT TGGAGATAAT GGAAATCGTA AAAAAACTAT GTTTGAGAAA 60

ATAACCTTGT TTATCGTGAT TATCATGCTA GTAGCAAGTT TATTGGGAAT TTTTGCAACT 120

GCAATTGGTG CCCTCAGTAA TCTATAAAAT AGATTCAAGA AAATTTAGTG ACTGGGATTT 180

CCCAGCCCTT TTTTAAAGTG AGAAGAAATA ATGAGTATGT TTTTAGATAC AGCTAAGATT 240

AAGGTCAAGG CTGGTAATGG TGGCGATGGT ATGGTTGCCT TTCGTCGTGA AAAATATGTC 300

CCTAATGGAG GCCCTTGGGG TGGTGATGGT GGTCGTGGAG GCAATGTGGT CTTCGTTGTA 360

GACGAAGGAC TACGTACCTT GATGGATTTC CGCTACAATC GTCATTTCAA GGCTGATTCT 420

GGTGAAAAAG GGATGACCAA AGGGATGCAT GGTCGTGGTG CTGAGGACCT TAGAGTTCGA 480

GTACCACAAG GTACGACTGT TCGTGATGCG GAGACTGGCA AGGTTTTAAC AGATTTGATT 540

GAACATGGGC AAGAATTTAT CGTTGCCCAC GGTGGTCGTG GTGGACGTGG AAATATTCGT 600

TTCGCGACAC CAAAAAATCC TGCACCGGAA ATCTCTGAAA ATGGAGAACC AGGTCAGGAA 660

CGTGAGTTAC AATTGGAACT AAAAATCTTG GCAGATGTCG GTTTAGTAGG ATTCCCATCT 720

GTAGGGAAGT CAACACTTTT AAGTGTTATT ACCTCAGCTA AGCCTAAAAT TGGTGCCTAC 780

CACTTTACCA CTATTGTACC AAATTTAGGT ATGGTTCGCA CCCAATCAGG TGAATCCTTT 840

GCAGTAGCCG ACTTGCCAGG TTTGATTGAA GGGGCTAGTC AAGGTGTTGG TTTGGGAACT 900

CAGTTCCTCC GTCACATCGA GCGTACACGT GTTATCCTTC ACATCATTGA TATGTCAGCT 960

AGCGAGGGCC GTGATCCATA TGAGGACTAC CTAGCTATCA ATAAAGAGCT GGAGTCTTAC 1020

AATCTTCGCC TCATGGAGCG TCCACAGATT ATTGTAGCTA ATAAGATGGA CATGCCTGAG 1080

AGTCAGGAAA ATCTTGAAGA CTTTAAGAAA AAATTGGCTG AAAATTATGA TGAATTTGAA 1140

GAGTTACCAG CTATCTTCCC AATTTCTGGA TTGACCAAGC AAGGTCTGGC AACACTTTTA 1200

GATGCTACAG CTGAATTGTT AGACAAGACA CCAGAATTTT TGCTCTACGA CGAGTCCGAT 1260

ATGGAAGAAG AAGCTTACTA TGGATTTGAC GAAGAAGAAA AAGCCTTTGA AATTAGTCGT 1320

GATGACGATG CGACATGGGT ACTTTCTGGT GAAAAACTCA TGAAACTCTT TAATATGACC 1380

AACTTTGATC GTGATGAATC TGTCATGAAA TTTGCCCGTC AGCTTCGTGG TATGGGGGTT 1440

GATGAAGCCC TTCGTGCGCG TGGAGCTAAA GATGGGGATT TGGTCCGCAT TGGTAAATTT 1500

GAGTTTGAAT TTGTAGACTA GGAGACTGGT ATGGGAGATA AACCGATATC TTTCCGAGAT 1560

GCGGATGGTA ATTTTGTTTC CGCCGCAGAC GTTTGGAATG AAAAGAAATT GGAAGAACTA 1620

TTTAATCGTC TCAATCCAAA TCGTGCCTTG AGATTGGCAC GAACTAAAAA GGAAAATCCA 1680

TCTCAGTAAA GAAGCTAAAA AATCCCGTGC CTCATCAGAC ACGGGATTTT GTGGTACGAC 1740

AGGCATGTAT AGCAAACTGA ATCTGGAATA GCACAGCATA TCTTCTAAAA TATAGTAAAA 1800

TGAAATGAGA ACAGGACAAA TCGATCAGGA CAGTAAAATC GATTTCTAAC AATGTTTTAT 1860

AAGCAGAGAT GTACTATTCT AGTTTCAATC AACTATATTG TTATAAATTG ATTTGAATTT 1920

CAAAATTAAA TTGTTTGATT CTTATTTCAA TTTGTTATAG TATATCTGAT GTCAAAGTTC 1980

TCGGCGAGTC AAATAGCGAT TCCCAAGCCT GACTATCGTG AGGTAGCGGA TTAAAATGGT 2040

CTGGGGATAG ACCGTTTTAA GTCTGACGCT GGAAATAAGA ATTGTCAGAA GAAGGGATAG 2100

CGAAATCGTG GCTCTACGAA CAGGAACGTG ATAATAAGGC GTATATAGCG GATAAGAGGG 2160

CATCAAACTC TAAAGTCCAA AAAGGTAGTC GTAACCTATA TGCGTAAATC ACGAGAGTAA 2220

TTGAATTCGT ACTAAGATTT TCTATTTTCA CTGTAACCTT TTAACGCCCT TATATCTTGT 2280

ATACACGAGG AAAGATGTAC GACTTATCCC GTGAGGTCTA TCACTATAAA GAGAAAACGA 2340

CAGATAGAAG TGATCCTGAG TCACGGTTAT CTGTCTGATA GGACGGTATG TATAAAACGC 2400

TTCTGTGAAC TGAGAGAAGG GGGAGAAGTT CTTGCTAAAA TTTAGTTGAA CAGCCGTATT 2460

CCGATACTTA GATAAGAGAT CTAGTCTTAG CTCCTACTCA GTTTTAGGGG ATAAAAAAGG 2520

GGCAATAGCG ATTCGAGAAA GATTATACTC TTCGAAAATC TCTTCAAATC ACGTCAATAT 2580

CGCCTTGTCG TATGTGTAGG ATACTGACTA CGTCAGTTCC ATCTACAACC TCAAAACAGT 2640

GTTTTGAGCA ACcTGCGGCT AGTTTCCTAG TTTGATCTTT GATTTTCATT GAGTATTAGT 2700

AATTCAGTTA CTAACTCGTC AACTCTGATT TATCCAATAA AATTGAAAAG GATGGAAAAA 2760

AGGATAAATT TATGATATAC TTTATTTTGA AGACCTTATT AGAAATCTTG AAAGAGTATT 2820

GAAAACTTAG AATGAGAAAA ATTGTTATCA ATGGTGGATT ACCACTGCAA GGTGAAATCA 2880

CTATTAGTGG TGCTAAAAAT AGTGTCGTTG CCTTAATTCC AGCTATTATC TTGGCTGATG 2940

ATGTGGTGAC TTTGGATTGC GTTCCAGATA TTTCGGATGT AGCCAGTCTT GTCGAAATCA 3000

TGGAATTGAT GGGAGCTACT GTTAAGCGTT ATGACGATGT ATTGGAGATT GACCCAAGAG 3060

GTGTTCAAAA TATTCCAATG CCTTATGGTA AAATTAACAG TCTTCGTGCA TCTTACTATT 3120

TTTATGGGAG CCTCTTAGGC CGTTTTGGTG AAGCGACAGT TGGTCTACCG GGAGGATGTG 3180

ATCTTGGTCC TCGTCCGATT GACTTACACC TTAAGGCGTT TGAAGCTATG GGTGCCACTG 3240

CTAGCTACGA GGGAGATAAC ATGAAGTTAT CTGCTAAAGA TACAGGACTT CATGGTGCAA 3300

GTATTTACAT GGATACGGTT AGTGTGGGAG CAACGATTAA TACGATGATT GCTGCGGTTA 3360

AAGCAAATGG TCGTACTATT ATTGAAAATG CAGCCCGTGA ACCTGAGATT ATTGATGTAG 3420

CTACTCTCTT GAATAATATG GGTGCCCATA TCCGTGGGGC AGGAACTAAT ATCATCATTA 3480
TTGATGGTGT TGAAAGATTA CATGGGACAC GTCATCAGGT GATTCCAGAC CGCATTGAAG 3540
CTGGAACATA TATATCTTTA GCTGCTGCAG TTGGTAAAGG AATTCGTATA AATAATGTTC 3600
TTTACGAACA CCTGGAAGGG TTTATTGCTA AGTTGGAAGA AATGGGAGTG AGAATGACTG 3660
TATCTGAAGA CAGCATTTTT GTCGAGGAAC AGTCTAATTT GAAAGCAATC AATATTAAGA 3720
CAGCTCCTTA CCCAGGCTTT GCAACTGATT TGCAACAACC GCTTACCCCT CTTTTACTAA 3780
GAGCGAATGG TCGTGGTACA ATTGTCGATA CGATTTACGA AAAACGTGTA AATCATGTTT 3840
TTGAACTAGC AAAGATGGAT GCGGATATTT CGACAACAAA TGGTCATATT TTGTACACGG 3900
GTGGACGTGA TTTACGTGGG GCCAGTGTTA AAGCGACCGA CTTAAGAGCT GGGGCTGCAC 3960
TAGTCATTGC TGGGCTTATG GCTGAAGGTA AAACTGAAAT TACCAATATC GAGTTTATCT 4020
TACGTGGTTA TTCTGATATT ATCGAAAAAT TACGTAATTT AGGAGCGGAT ATTAGACTTG 4080
TTGAGGATTA AACCGTAGAG GTGTTTATGA ATATTTGGAC CAAATTAGCA ATGTTTTCTT 4140
TTTTTGAAAC GGATCGCTTG TATTTGCGTC CTTTCTTTTT TAGTGATAGT CAGGACTTCC 4200
GCGAGATAGC TTCAAATCCA GAAAATCTTC AATTTATTTT CCCAACGCAG GCAAGTCTGG 4260
AAGAAAGTCA ATATGCACTG GCCAATTACT TTATGAAGTC CCCTTTGGGA GTGTGGGCAA 4320
TTTGTGACCA GAAAAATCAA CAAATGATTG GTTCTATTAA ATTTGAGAAG TTAGATGAAA 4380
TCAAAAAAGA AGCTGAGCTT GGCTATTTTT TGAGAAAAGA TGCTTGGTCG CAAGGATTTA 4440
TGACAGAGGT TGTTAGAAAA ATTTGTCAGC TTTCTTTTGA GGAATTTGGC TTAAAACAAT 4500
TATTTATCAT TACCCACCTT GAAAATAAAG CTAGCCAAAG AGTTGCTCTT AAGTCTGGAT 4560
TTAGTTTGTT CCGTCAGTTT AAGGGAAGTG ATCGTTACAC AAGAAAAATG CGGGATTATC 4620
TTGAATTTCG GTATGTAAAA GGAGAGTTCA ATGAGTAAGC ATCAGGAAAT TCTAAGCTAT 4680
TTGGAGGAAT TACCAGTAGG TAAAAGGGTC AGTGTTCGTA GCATTTCGAA TCATCTAGGA 4740
GTTAGTGATG GAACAGCCTA TCGGGCTATT AAAGAAGCTG AAAACCGTGG AATTGTGGAG 4800
ACCCGTCCTA GAAGTGGAAC AATTCGTGTT AAATCCCAGA AAGTTGCTAT AGAGAGATTA 4860
ACGTTTGCTG AAATTGCAGA AGTGACTTCT TCTGAGGTTC TGGCTGGGCA AGAAGGTTTA 4920
GAGAGAGAAT TTAGTAAGTT TTCAATTGGT GCCATGACTG AACAAAATAT CTTGTCTTAC 4980
CTTCATGATG GGGGGCTCTT GATTGTCGGA GACCGAACCC GTATTCAGTT GCTAGCCTTG 5040
GAAAATGAAA ATGCAGTTCT GGTTACAGGG GGATTTCAGG TTCATGATGA TGTGCTTAAA 5100
CTGGCCAATC AAAAAGGGAT TCCTGTTCTA AGAAGTAAGC ATGATACCTT TACCGTCGCG 5160

ACCATGATCA ATAAAGCCTT GTCAAATGTC CAAATCAAGA CTGATATTCT GACAGTTGAG 5220

AAACTTTATC GCCCTAGTCA TGAGTATGGT TTTCTGAGAG AGACAGATAC AGTTAAAGAT 5280

TATTTGGACT TGGTTCGTAA GAATCGTAGC AGCCGTTTCC CTGTTATCAA TCAACATCAG 5340

GTCGTTGTTG GTGTTGTAAC CATGAGAGAC GCTGGTGATA AATCACCAAG CACGACAATT 5400

GATAAGGTTA TGTCTCGTAG TCTATTTTTG GTTGGATTAT CGACAAATAT TGCCAATGTG 5460

AGTCAACGGA TGATCGCAGA AGACTTTGAA ATGGTACCAG TTGTTCGAAG CAATCAAACT 5520

TTGCTTGGCG TTGTGACGCG ACGAGATGTC ATGGAGAAGA TGAGCCGTTC CCAAGTTTCG 5580

GCTCTACCAA CTTTTTCTGA GCAGATTGGA CAAAAGCTCT CTTATCACCA TGATGAAGTA 5640

GTCATTACAG TGGAACCCTT TATGCTAGAA AAAAATGGAG TTTTGGCTAA TGGTGTATTG 5700

GCAGAAATTC TGACCCACAT GACCCGATTT AGTTGTTAAT AGTGGTCGCA ATCTCATTAT 5760

CGAGCAGATG CTGATCTACT TTTTGCAGGC TGTTCAGATA GATGATATAT TGCGCATTCA 5820

GGCACGGATT ATTCATCATA CGAGACGGTC AGCTATAATT GATTACGATA TTTATCATGG 5880

TCACCAGATT GTTTCAAAAG CAAATGTGAC TGTTAAAATT AATTAGAAAC TAGGAGAAAA 5940

GATGATAACA TTAAAATCAG CTCGTGAAAT CGAAGCTATG GACAAGGCTG GTGATTTTCT 6000

AGCAAGTATT CATATAGGCT TACGTGATTT GATTAAGCCA GGCGTAGATA TGTGGGAAGT 6060

TGAAGAATAT GTCCGCCGTC GTTGTAAAGA AGAAAATTTC CTTCCACTTC AGATTGGGGT 6120

TGACGGTGCC ATGATGGACT ATCCTTATGC TACCTGTTGC TCTCTTAACG ATGAAGTGGC 6180

TCACGCTTTC CCTCGTCATT ATATCTTGAA AGATGGTGAT TTGCTCAAAG TTGATATGGT 6240

TTTGGGAGGT CCCATTGCTA AATCTGACCT AAATGTCTCA AAATTAAACT TCAACAATGT 6300

TGAACAAATG AAAAAATACA CTCAGAGCTA TTCTGGTGGT TTAGCAGACT CATGTTGGGC 6360

TTATGCTGTT GGTACACCGT CCGAAGAAGT CAAAAACTTG ATGGATGTAA CCAAAGAAGC 6420

TATGTACAAG GGTATTGAGC AAGCTGTTGT TGGAAATCGT ATCGGTGATA TCGGTGCGGC 6480

TATTCAAGAA TACGCTGAAA GTCGTGGTTA CGGTGTAGTG CGTGATTTGG TTGGTCATGG 6540

TGTTGGCCCA ACTATGCACG AAGAACCAAT GGTTCCTAAC TATGGTATTG CAGGTCGTGG 6600

ACTCCGTCTT CGTGAAGGAA TGGTCTTAAC CATTGAACCA ATGATCAATA CAGGCGATTG 6660

GGAAATTGAT ACAGATATGA AAACTGGTTG GGCGCATAAG ACCATTGACG GTGGATTGTC 6720

ATGTCAGTAT GAACACCAAT TTGTCATTAC GAAAGATGGA CCTGTTATCT TGACTAGCCA 6780

AGGTGAAGAA GGAACTTATT AATAAAAAGT GAAAAGACTA CTGGAAGTTT ATTTTGATAA 6840

AAAATCCAGT AGATCTTTTC ATAATAAAAC GCATTGTATC AAGTGTTAGG GGCTGATATC 6900

ATGCGTTTTT CTGCTTTTAA GATTTTTTCC AACTCTGTTT GTAAGCGCAT CATAACAAAG 6960

GGTCTAGGAT TCAGGGCTCT CCTCCTATAT ACTATTAGTA AAGTAAAACT AAGGGAGGAT 7020

ATTTTAGTGT CGCAGTCTAT TGTTCCTGTA GAGATTCCAC AATATTGTCG TTTTGATTCT 7080

AAAAAGAGAA ATGGAATTCT GTTTAATGTT CGTATTGCCA ATCTTAAATT TACTTTTTTA 7140

TATTATACTT CCTGCGAAAC AAAATATGGT ATAGTAGTTC TATGAATGAT GAAGCAAGTA 7200

AACAACTAAC TGATGCACGA TTTAAGCGTC TTGTTGGTGT TCAGCGTACC ACTTTTGAAG 7260

AGATGTTAGC TGTATTAAAA ACAGCTTATC AACTTAAACA CGCAAAAGGT GGACGAAAAC 7320

CTAAATTAAG CCTAGAAGAC CTTCTTATGC CCACTCTTCA ATAGTGCGAG AATATCGAAC 7380

TTATGAAGAA ATTGCGGCTG ATTTTGGTAT TCACGAAAGC AACTTTATCC GTCGGAGCCA 7440

ATGGGTTGAA ATAACTCTTG TTCAAAGTGG TTTTACGGTT TCAAGAACTC CTCTCAGTTC 7500

TGAGGACACG GTAATGATTG ATGCGACGGA AGTAAAAATC AATCGCCCTA AAAAAACAAT 7560

TAGCGAATGA TTCTGGTAAA AAGAAATTTC ACGCTATGAA GGCTCAAGCG ATTGTCACAA 7620

GTCAAGGGAG AATTGTTTCT TTGGATATCG CTGTGAACTA TAGTCATGAT ATGAAGTTGT 7680

TCAAAATGAG TCGTAGAAAT ATCGAACAAG CTGGTAAAAT CTTGGCTGAC AGTGGTTATC 7740

AAGGGCTCAT GAAGATATAT CCTCAAGCAC AAACTCCACG TAAATCCAGC AAACTCAAGC 7800

CGCTAACAGC TGAAGATAAA GCCTATAACC ATGCGCTATC TAAGGAAAGA AGCAAGGTTG 7860

AGAACATCTT TGCCAAAGTA AAAACGTTTA AAATATTTTC AACAACCTAT CGAAATCATC 7920

GTAAACGCTT CGGATTACGA ATGAATTTGA GTGCTGGTAT TATCAATCAT GAACTAGGAT 7980

TCTAGTTTTG CAGGAAGTCT ATTGAGGTAT TGAGCTAGTT TATGAAAAAA TTGGGTGAAA 8040

AGTCGAGTGT TTTAGAAACC CACAGTGTAG TATTCTAGTT TCAATCCACT ATATTTTGCT 8100

ACTCCCCGTA AAGTTTCTAT TTTCCCTGAT TTCTGATATA ATAGAAATAT TGACTTCAAG 8160

AGTAAGGAAG AGAAGATGAA CGCATTATTA AATGGAATGA ATGACCGTCA GGCTGAGGCG 8220

GTGCAAACGA CAGAAGGTCC CTTGCTAATC ATGGCAGGGG CTGGTTCTGG AAAGACTCGT 8280

GTTTTGACCC ACCGTATCGC TTATTTGATT GATGAAAAGC TGGTCAATCC TTGGAATATC 8340

TTGGCCATTA CCTTTACCAA CAAGGCTGCG CGTGAGATGA AAGAGCGTGC TTATAGCCTC 8400

AATCCAGCGA CTCAGGACTG TCTGATTGCG ACCTTCCACT CCATGTGTGT GCGTATTTTG 8460

CGTCGCGATG CGGACCATAT TGGCTACAAT CGTAATTTTA CAATTGTGGA TCCTGGTGAA 8520

CAGCGAACGC TCATGAAACG TATTCTCAAA CAGTTGAACT TGGACCCTAA AAAATGGAAT 8580

GAACGAACTA TTTTGGGGAC CATTTCCAAT GCTAAGAATG ATTTGATTGA TGATGTTGCT 8640

TATGCTGCCC AAGCTGGCGA TATGTATACG CAAATTGTGG CCCAGTGTTA TACAGCCTAT 8700

CAAAAAGAAC TTCGTCAGTC TGAATCCGTT GACTTTGATG ATTTGATTAT GCTGACCTTG 8760

CGTCTCTTTG ATCAAAATCC TGATGTTTTG ACCTACTACC AGCAAAAATT CCAATACATC 8820

CACGTTGATG AGTACCAAGA TACCAACCAC GCTCAGTACC AATTGGTCAA ACTCTTGGCT 8880

TCCCGTTTTA AAAATATCTG TGTGGTTGGG GATGCGGACC AGTCTATCTA CGGTTGGCGT 8940

GGTGCTGATA TGCAGAATAT CTTGGACTTT GAAAAGGATT ACCCCAAAGC CAAGGTTGTT 9000

TTGTTGGAGG AAAATTACCG CTCAACCAAA ACCATTCTCC AAGCGGCCAA CGAGGTTATT 9060

AAAAATAATA AAAATCGCCG TCCTAAAAAT CTCTGGACTC AAAACGCTGA TGGGGAGCAA 9120

ATCGTTTACT ATCGTGCCGA TGATGAGCTG GATGAGGCTG TATTTGTAGC CAGAACCATC 9180

GATGAACTTA GTCGCAGTCA AAACTTCCTT CATAAGGATT TTGCAGTTCT CTATCGGACT 9240

AATGCCCAGT CCCGTACAAT TGAGGAAGCC CTGCTCAAGT CTAACATTCC TTATACCATG 9300

GTTGGCGGAA CCAAATTCTA CAGCCGTAAG GAAATTCGCG ATATTATTGC TTATCTCAAC 9360

CTTATTGCTA ATTTGAGTGA CAATATTAGT TTTGAGCGTA TTATCAACGA GCCTAAACGT 9420

GGAATTGGTC TAGGTACAGT TGAGAAAATC CGTGATTTTG CAAATTTGCA AAATATGTCT 9480

ATGCTGGATG CTTCTGCTAA TATTATGTTG TCTGGTATCA AGGGTAAGGC AGCCCAATCT 9540

ATCTGGGATT TTGCCAATAT GATGCTTGAT TTGCGGGAGC AGCTAGACCA CTTAAGCATT 9600

ACAGAGTTGG TTGAGTCCGT CCTAGAAAAA ACAGGTTATG TCGATATTCT TAACTCCCAA 9660

GCGACTCTAG AAAGCAAGGC ACGGGTTGAA AATATCGAAG AGTTTCTTTC TGTTACGAAG 9720

AACTTTGATG ACACCACGGA TGTGACAGAA GAGGAAACTG GTCTGGACAA ACTGAGTCGT 9780

TTCTTAAATG ACTTGGCTTT GATTGCCGAC ACAGATTCAG GTAGTCAGGA GACATCAGAA 9840

GTGACCTTGA TGACCCTGCA TGCTGCCAAA GGTCTCGAAT TTCCAGTTGT CTTTTTGATT 9900

GGGATGGAAG AAAATGTCTT TCCACTTAGT CGTGCGACTG AAGATTCAGA TGAATTAGAA 9960

GAAGAGCGCC GTCTAGCCTA TGTAGGTATC ACGCGTGCAG AGAAAATTCT CTATCTGACC 10020

AATGCCAACT CACGCTTGCT TTTTGGTCGT ACCAATTATA ACCGTCCGAC TCGTTTTATT 10080

AACGAAATCA GTTCAGACTT GCTTGAGTAT CAAGGTCTGG CTCGTCCTGC AAATACAAGC 10140

TTTAAGGCAT CATATAGCAG TGGTAGTATT TCCTTTGGTC AAGGTATGAG TTTGGCTCAG 10200

GCTCTTCAAG ACCGTAAACG CGGTGCTGCC CCAAAATCAA TCCAGTCAAG CGGTCTTCCA 10260

TTTGGTCAAT TTACAGCTGG CGCAAAACCA GCATCTAGCG AGGCAAATTG GTCCATTGGT 10320

GATATTGCTC TCCACAAGAA ATGGGGAGAG GGAACCGTTC TGGAAGTTTC AGGTAGCGGT 10380

GCTAGGCAGG AATTGAAAAT CAATTTCCCA GAAGTAGGTT TGAAAAAACT TTTAGCCAGT 10440

GTGGCTCCAA TTGAGAAAAA AATCTAATTT TCCATCCTTC TCACGAATAA TAAAGTGAGG 10500

AGGATTTTTA TGTACAGTAT TTCATTCCAA GAAGATTCAC TATTACCAAG AGAAAGGCTG 10560
GCCAAGGAAG GAGTTGAAGC GCTTAGTAAC CAAGAGTTGC TAGCTATTTT ACTCAGGACA 10620
GGAACACGTC AAGCTAGCGT TTTTGAAATT GCCCAAAAAG TCTTGAACAA TCTTTCAAGC 10680
CTAACGGATT TGAAAAAAAT GACCCTGCAG GAATTGCAGA GTTTGTCTGG TATTGGGCGT 10740
GTTAAGGCCA TAGAATTACA AGCTATGATT GAACTGGGGC ATCGTATTCA CAAACACGAG 10800
ACTCTTGAAA TGGAAAGTAT TCTCAGCAGT CAAAAGTTGG CCAAGAAGAT GCAGCAGGAA 10860
TTAGGGGATA AAAAACAAGA GCACCTGGTG GCACTCTATC TCAATACTCA AAATCAAATC 10920
ATCCATCAGC AGACCATTTT TATCGGGTCT GTAACTCGTA GTATCGCTGA ACCGCGAGAG 10980
ATTCTTCACT ATGCAATCAA GCATATGGCG ACTTCTCTTA TCTTGGTCCA CAATCATCCT 11040
TCAGGAGCGG TAGCGCCTAG CCAAAATGAT GATCATGTCA CTAAACTTGT TAAAGAAGCC 11100
TGCGAATTGA TGGGGATTGT TCTCTTGGAC CATTTGATTG TCTCTCATTC TAATTACTTT 11160
AGTTATCGTG AAAAGACAGA TTTAATCTAA AGTTCATTAA CGACATAGTC AAAGAGTTTT 11220
TTATCTTTGG GACGATTTTC AAAAAGAAGT TCTGGATGCC ATTGGACACC GAGAAAGGCG 11280
ACATCATCCG TACTCATGAC AGCCTCAATG ATACCATCTT TAGGATCATG AGCCACAACT 11340
TTTAAATTTG GTGCTAAGTC CTTGATGCTC TGGTGGTGGA AGGAGTTGAT ATGAGAGATT 11400
TCTCCATAGA TTTCTTGGAG AACGGTATCT GGTTCTGTTA CCAAGCGTTG AGTTGTGTAC 11460
TCAACAGAAG AATCCTGCCA ATGGTCTTCG ATATCTTGGT ACAAAGTTCC ACCCATGGCA 11520
ACGTTAAAGA GTTGGGTACC ACGGCAGACA GAGAAAATGG GCTTTTTCTG TTTAATAGCT 11580
TCCTTGATGA GGGCCAGTTC GAAGATATCT CTTTGAAGGT GATAGTCATC ACTATCAATG 11640
GTTTTGGGTT CGCCATAAAA TTTTGGATCG ACATTTTGCC CACCTGTCAA GATGAGCTTG 11700
TCAATCAAAC TGATATAGTG GCAGGCCATT TCTTGATCAC CAATCGGTAG GATGATGGGA 11760
ATCCCTCCAG CATCTTTAAC GCCTTCAACA AAGCCTTTTG CTGCGTAGCT CATCATGATG 11820
TCATCATCTG GATGAGTTTT TTCGTTTCCT GTAATCCCAA TAACTGGTTT TTTCATAAAA 11880
TGATTTTCGC TTTCTAATCC TCTTTTCGCA TGAAGTAGAG GAGGGTTTGG AGTTCACTTG 11940
TCAAATCGAC ATACTGAACG ACCACGTCTT TTGGTAAATG CAGATGGACT GGTGAAAAAC 12000
TGAGAATTCC TTTCACACCA GCATCAACCA AGAGATTAGC AACCTCTTGT GACTTGACGC 12060
TGGGAACAGT TAGGATAGCA GTCTTCACAT CAGCATCCTT GATTTTATCC TTGATCTGAG 12120
AAATCCCGTA AATGGGAATC CCGTCAGGAG TTTGGGTACC GACTTCAGGA TGGTCGTCTA 12180
GGTCAAAGGC CATGATAATC TTCATCTTGT TACGTTCGTG GAAGCGGTAG TGGAGAAGGG 12240

CATGGCCCAT ATTTCCAATA CCAACCAGCA TGACATTGGT AATAGAGTTG TCATTGAGCA 12300

AATCGGCAAA AAATGTCATT AGTTTTTTGA CATCATAGCC AAAACCACGA CGACCAAGTT 12360

CACCAAAATA GGAAAAATCA CGACGTACGG TCGCTGAATC AATACCGATA GCCTCTGCAA 12420

TTTGCTTAGA GTTGGCACGT TCAATCTTTT CTGCATGAAA TCTCTTAAAA ATTCGATAGT 12480

AGAGAGAGAG TCTTTTTGCT GTAGCTTTTG GAATAGCAAA CTGTTTATCT TTCACAAAAT 12540

CACAACCTTT CTATTCTTCT ATTTTATAGA AACATTGTGA AAAAATCAAC AAAAATAAGA 12600

AAAAACTAAG AAAAATCTTA GTTTTGATGT AAAAAATCTG CATGAGATAG AAAACGGTAG 12660

AGGTCTCCGA CCAGCCCCTG ATAAACTTTT TTGCCCCTAA AAGTCAGAGA AGTCACATAA 12720

AGTGTATCTG GTAAGGTTAC ACATCCTGAC AAAGTCAACA TGAGAGCCTC ATGATCCTCA 12780

TACTTGAGAG TACGCTCTAC ATGATAGCAG TCCTTATAGG TCAGTTCAAA CATTTTGGCT 12840

CTATCTTTCC GATTTTGTAA AGACACCACG TTCTACCAAG CTATCCATGA GGAAGTAGAA 12900

TTTTTCCTGA TGAATATGGT GGTCTTCTGA TTTGAAAATA TCAACTAGAC GAAGGCCAAA 12960

CTTGTCAGTG ATATTGATTT TAGCCCCTGT AAGTTCCTTG TTAATGATGA TTTTGAGTTG 13020

GAAGCCTTCA CCGCTGTTTG GCACTTTTTC CAAAAGGCGA GTCAGTTCAT AGTTACCAAC 13080

CTTAGTTTCA AAAAAGGTGT TATCTTTGAG GGTGAATTTT TTAACAGAAG GGCTAAGAGT 13140

GTAATCGTAA CGACAATTTT TTAACTGAAT GATTTTTTCA AATGCCATAT GGCTAACCTC 13200

CGATAATTTC TTTTAAGGTT TTTGCGAGGG TTTGTAGGTC TTCAACGGTA TTTTGTGGCG 13260

ACAAACTGAT GCGAAGGGAT TCCTTCAAGC GTTCTGAATT TGCGCCATAC ATGGCTTCAA 13320

GAACATGGCT GGATTGGACA ACGCCTGCAG TACAGGCTGA GCCAGTAGAG ATTGAAATTC 13380

CAGCTAAATC TAGCCGAAGG AGTAAGAGGT CATTTTTCTG ACCAGGAAAT CCAATATTGA 13440

GAACATAAGG GAGATGATGT TTTCCTCTAT TCAGGTAATA CTGAATGCCC TCCAGCTCTG 13500

CCAGAAAGGC AGTTTCTAGA TTTTGTACAT GTTGAAAATG TTCTTCTTGT TTTTCTAGGT 13560

CTTCTTTTAG GGCTGCAACC ATGCCTACAA TGGCAGGCAG ATTTTCAGTT CCTGCACGTT 13620

TTTTCTGTTC CTGGTCTCCG CCATGTAGAT AGGAATCAAA GTCCATGCTA GATGCGTAGA 13680

GAAAACCGAT TCCCTTAGGA CCATGGAATT TGTGGGCAGA AGCAGTGAGA AAATCAATGC 13740

CCAATTCTTC TGAATGAATT GGGATTTTAC CAATAGCCTG AACTGCATCA ACATGATAGG 13800

CAGCAGGGTG TTGCTTGAGT ATTTGGCCAA TTTCAGCGAT GGGCAGTAGG TTTCCTGTCT 13860

CATTATTGAC AAACATGGTA GAAACCAAAA TCGTATCGTC ACGTAAAGCC TTTTGAATTT 13920

GCTGGGCTGT GATTTCTTGA TTTTCTGGCT GGATAATGGT TGCTTCAAAC CCAAAGTGTT 13980

GAACCAAGTA ATCAATTGTT TCAAGGACAG CATGGTGCTC GATGGCAGTT GTGATGATAT 14040

GTTTTCCTTG TTCTTGGTGA CGAAGACAGT AGCCAATGAT GGTAGTATTA TTGCCTTCAG 14100
TCCCACCAGA AGTGAAAAAG ATATGTTGAG GTTTTGTCCT TAGTAACTGG GCTAGTTCCT 14160
GACGGGCTTC TCGCAAGAGT TTGCCAGCTT GACGACCATG ACCATGAATA CTAGAAGGAT 14220
TTCCGTGGGT TTCTTGCATA ACCTTGGTCA TAGCTGAAAT AGCAACTGCT GACATAGGAG 14280
TCGTTGCAGC ATTGTCCAAA TAAATCAAAG AATCACCTTA TTTCTTTTTA TTGTAGGCAA 14340
AGAGTGGGCT GACTGGTTTT CTTTCGTGAA TACGGACGAT AGCATCACCA ATTAACTCAC 14400
TAGCAGTGAT GTAGCATACA TTTTTAGGAG TTTTTTCTTT TGTTGCTACT GAATCAGTCA 14460
CAAGAATTTC TTTAATATTA GTATTGTCAA GAAGCTCAGC AGCTCCCTCG ACGAAGAGAC 14520
CGTGGCTAGA AACAGCATAA ATTTCTGTAG CTCCTTCACG TTCAACGATT TTAGAAGCTT 14580
CAGAGAAGGT ACGTCCTGTA TTTAAAATAT CATCAATCAA GATAGCTTTC TTACCTTCAA 14640
CATCACCAAT AATATAACCT TCGTTACGAG TTGCATCGTC TTGAGGGTAG TCGATAATGG 14700
CGATAGGAGC ATCAAGATAT TCAGCCAGGC TACGCGCACG TTTGACACCT GAATTTTTAG 14760
GGCTAACGAC AACAACATCT GAACCAAGCA ATCCTTTATC GCAGTAATGT TTTGCGAATA 14820
GGGGAACAGT GAAAAGATTA TCCACTGGAA TATCAAAGAA ACCTTGAACC TGAACGGCAT 14880
GCAAATCAAG AGTCAGGATA CGATCAACTC CAGCCTTAAC CAGCATATTG GCAACTAGTT 14940
TTGCTGTAAG TGGCTCACGA GGACAAGCAA TGCGGTCTTG ACGTGCATAG CCAAAATATG 15000
GAAGGACAAC GTTGATACTG TGGGCACTTG CACGCACACA AGCATCGACC ATGATTAACA 15060
ATTCCATTAG GTGGTTGTTG ACAGGGAAAC TTGTTGATTG GATGATGTAA ACATCATAAC 15120
CACGGACACT TTCTTCGATA TTTACTTGGA TTTCTCCGTC TGAAAATTGA CGTGATGATA 15180
GTTTTCCAAG TGGGACACCA ACAGCTTGGG CAATTTTTTG TGCAATCTCT TGGTTAGAGT 15240
TGAGTGCGAA AAGTTTCATG TTTTTTCTAT CTGACATTAT AGACCGTCCT CTGTAAACTT 15300
TATAAATCCT AGTTATATTT ACCTTACATA TATGAACTGG GATTTGTGTA TTTTTATCTT 15360
TTCTATTTTA CCAAAAAATG GAGATTATTT CAGCTATTTT TCATACTTTT GACAAATCGA 15420
ACCAATTTTG AAGGAGCTTT TTGATAGGAA ATCTGATTTT TCTCTAAAAA TTGTCGAAAA 15480
TCCTGTTTGC CTTGCTCATG ATTTTCCACT TCAAGCTCCA ATTCGTAATC TGTTATATCA 15540
AAGTATCGGC TCTGATCCAG TGCCATGAGA CCAATAGCTG TTTTCATTTC ATAGCGAAGC 15600
GTTGTTAGAC AACCAAGAAC CTGCCAGTTC TTACTTTGGA TACCATGTTT CGCCAATTCA 15660
TCCAGTACTA GCCCTTGAGG AAGTTCTTCC TTACTCAGAT AGTTCTCAGC ATCTTTTAGT 15720
TGCAATTTTT GGTTGTATTC CATGTTTCCA ACACTCTGCG GGACTTTGAG TGTCAACTCA 15780

GCCCAGTCTT CAAAGGTTCG AATGCGCATA GCGACTTTCT TTTCTCGCAG TTCAAAATCA 15840

GGCGTGTCGA TGTAGTAATT TGTTTGAAGA ACAGGAGTGA CACCTGTGAA CTGGTCTTTT 15900

AGACGATTGT ATTCATCTTT TTTCAATAGT GTTTTCAATT CAATTTCTAA ATGTTTCATT 15960

TTTCTTACCT TTTTTTATCG TTGAAAGCGG ATTTATGGTA TAATAAGCAT TGTATTTATT 16020

GTATATGAAT CTGGAGAAAA AATCAAAGAT ATTTTTGACG GATAATATGA GAACAAGGGA 16080

GAATATATGA CCTTAGAATG GGAAGAATTT CTAGATCCTT ACATTCAAGC TGTTGGTGAG 16140

TTAAAGATTA AACTTCGTGG TATTCGTAAG CAATATCGTA AGCAAAATAA GCATTCTCCA 16200

ATTGAGTTTG TGACCGGTCG AGTCAAGCCA ATTGAGAGCA TCAAAGAAAA AATGGCTCGT 16260

CGTGGCATTA CTTATGCGAC CTTGGAACAC GATTTGCAGG ATATTGCTGG CTTACGTGTG 16320

ATGGTTCAGT TTGTAGATGA CGTCAAGGAA GTAGTGGATA TTTTGCACAA GCGTCAGGAT 16380

ATGCGAATCA TACAGGAGCG AGATTACATT ACTCATAGAA AAGCATCAGG CTATCGTTCC 16440

TATCATGTGG TAGTAGAATA TACGGTTGAT ACCATCAATG GAGCTAAGAC TATTTTGGCA 16500

GAAATTCAAA TTCGTACTTT GGCCATGAAT TTCTGGGCAA CGATAGAACA TTCTCTCAAC 16560

TACAAGTACC AAGGGGATTT CCCAGATGAG ATTAAGAAGC GACTGGAAAT TACAGCTAGA 16620

ATCGCCCATC AGTTGGATGA AGAAATGGGT GAAATTCGTG ATGATATCCA AGAAGCCCAG 16680

GCACTTTTTG ATCCTTTGAG TAGAAAATTA AATGACGGTG TAGGAAACAG TGACGATACA 16740

GATGAAGAAT ACAGGTAAAC GAATTGATCT GATAGCCAAT AGAAAACCGC AGAGTCAAAG 16800

GGTTTTGTAT GAATTGCGAG ATCGTTTGAA GAGAAATCAG TTTATACTCA ATGATACCAA 16860

TCCGGATATT GTCATTTCCA TTGGCGGGGA TGGTATGCTC TTGTCGGCCT TTCATAAGTA 16920

CGAAAATCAG CTTGACAAGG TCCGCTTTAT CGGTCTTCAT ACTGGACATT TGGGCTTCTA 16980

TACAGATTAT CGTGATTTTG AGTTGGACAA GCTAGTGACT AATTTGCAGC TAGATACTGG 17040

GGCAAGGGTT TCTTACCCTG TTCTGAATGT GAAGGTCTTT CTTGAAAATG GTGAAGTTAA 17100

GATTTTCAGA GCACTCAACG AAGCCAGCAT CCGCAGGTCT GATCGAACCA TGGTGGCAGA 17160

TATTGTAATA AATGGTGTTC CCTTTGAACG TTTTCGTGGA GACGGGCTAA CAGTTTCGAC 17220

ACCGACTGGT AGTACTGCCT ATAACAAGTC TCTTGGCGGT GCTGTTTTAC ACCCTACCAT 17280

TGAAGCTTTG CAATTAACGG AAATTGCCAG CCTTAATAAT CGTGTCTATC GAACACTGGG 17340

CTCTTCCATT ATTGTGCCTA AGAAGGATAA GATTGAACTT ATTCCAACAA GAAACGATTA 17400

TCATACTATT TCGGTTGACA ATAGCGTTTA TTCTTTCCGT AATATTGAGC GTATTGAGTA 17460

TCAAATCGAC CATCATAAGA TTCACTTTGT CGCGACTCCT AGCCATACCA GTTTCTGGAA 17520

CCGTGTTAAG GACGCCTTTA TCGGCGAGGT GGATGAATGA GGTTTGAATT TATCGCAGAT 17580

GAACATGTCA AGGTTAAGAC CTTCTTAAAA AAGCACGAGG TTTCTAAGGG ATTGCTGGCC 17640

AAGATTAAGT TTCGAGGTGG AGCTATTCTG GTCAATAATC AACCGCAAAA TGCAACGTAT 17700

CTATTGGACG TTGGAGACTA CGTTACCATT GACATTCCCG CTGAGAAAGG CTTTGAAACC 17760

TTGGAGGCTA TTGAGCTTCC ATTAGATATT CTCTATGAGG ATGACCACTT TCTAGTCTTG 17820

AATAAACCCT ATGGAGTGGC TTCTATTCCT AGTGTCAATC ACTCTAATAC CATTGCCAAT 17880

TTTATCAAGG GTTACTATGT CAAGCAAAAT TATGAAAATC AGCAGGTTCA CATTGTTACC 17940

AGACTAGATA GGGATACTTC TGGCTTGATG CTCTTTGCCA AGCACGGTTA TGCCCATGCA 18000

CGATTAGACA AGCAGTTGCA GAAGAAATCT ATCGAGAAAC GCTACTTTGC TTTGGTTAAG 18060

GGAGATGGAC ATTTGGAGCC AGAAGGGGAA ATTATTGCTC CGATTGCGCG TGATGAAGAT 18120

TCCATTATTA CCAGACGAGT GGCTAAAGGC GGAAAGTATG CCCATACTTC ATACAAGATT 18180

GTAGCTTCTT ATGGAAATAT TCACTTGGTC TATATTCACC TGCACACTGG TCGAACCCAT 18240

CAAATCCGAG TCCATTTTTC TCATATCGGT TTTCCTTTGC TGGGAGATGA TTTGTATGGT 18300

GGTAGTCTGG AAGATGGTAT TCAACGTCAG GCTCTGCATT GCCATTACCT ATCCTTTTAT 18360

CATCCATTTT TAGAGCAAGA CTTGCAGTTA GAAAGTCCCT TGCCGGATGA TTTTAGTAAC 18420

CTTATTACCC AGTTATCAAC TAATACTCTA TAAAAACTGT CTCAGAGTAT AATTATTATC 18480

TTAAAGGAGA AAACTCATGG AAGTTTTTGA AAGTCTCAAA GCCAACCTTG TTGGTAAAAA 18540

TGCTCGTATC GTTCTCCCTG AAGGGGAAGA GCCTCGTATT CTTCAAGCAA CAAAACGCTT 18600

AGTAAAAGAA ACAGAAGTGA TTCCTGTTTT GCTTGGAAAT CCTGAAAAAA TTAAAATTTA 18660

TCTTGAAATT GAAGGAATCA TGGATGGTTA TGAGGTCATC GACCCTCAAC ATTATCCTCA 18720

ATTTGAAGAA ATGGTTTCTG CCTTGGTGGA GCGTCGCAAG GGCAAAATGA CTGAAGAAGA 18780

TGTACGCAAG GTTTTGGTTG AAGATGTCAA CTACTTTGGT GTGATGTTGG TTTACTTGGG 18840

CTTGGTTGAT GGAATGGTGT CAGGAGCGAT TCACTCAACA GCTTCAACAG TTCGCCCAGC 18900

TCTACAAATC ATCAAAACTC GTCCAAATGT AACTCGTACT TCAGGAGCCT TCCTCATGGT 18960

TCGTGGTACG GAACGTTACC TATTTGGAGA CTGTGCCATT AACATCAATC CAGATGCAGA 19020

AGCCTTGGCT GAAATTGCCA TCAACTCAGC AATCACAGCT AAGATGTTTG GCATCGAACC 19080

TAAAATTGCC ATGTTGAGCT ATTCTACTAA AGGTTCAGGG TTTGGTGAAA GCGTTGATAA 19140

GGTCGTTGAA GCAACTAAAA TTGCTCACGA CTTGCGTCCT GACCTTGAAA TCGATGGTGA 19200

GTTGCAATTT GATGCAGCCT TTGTTCCTGA AACTGCAGCT CTGAAAGCTC CTGGAAGTAC 19260

GGTAGCTGGT CAAGCAAATG TCTTCATCTT CCCAGGTATC GAGGCAGGAA ATATTGGTTA 19320

CAAGATGGCT GAACGCCTGG GTGGCTTTGC GGCTGTAGGA CCTGTTTTGC AAGGTTTAAA 19380

CAAGCCAGTT AATGATCTTT CTCGTGGATG TAATGCAGAT GATGTTTACA AGTTGACCCT 19440

CATCACAGCA GCTCAAGCAG TTCATCAATA GTGAAAACTA TAAAGTGATA TACTATGCTA 19500

TACTGTAGTT ATGAAACTAT GTACGAAAAG CACTGCCATT AATTCCTGAG AACTAAATTA 19560

CTGATTGGTG TCAAAAAGGA AAACTTCCAA GCGATGATAT CCTGTCTATA CACGACCTAT 19620

AGAAATCTGT AATATACATA TCCGTAAAAC GATAAATTCC CTTTTTGATT TTAAATGAGT 19680

ATGAAAAGAG AATTTTTTGG CTCTTTGTCA ACTGTAGTGG GTTGAAGAAA AGCTAAGCTC 19740

GAGAAAGGAC AAATTTCATC CTTTCTTTTT TGATATTCAG AGCGATAAAA ATCCGTTTTT 19800

TGAAGTTTTC AAAGTTCCGA AAACCAAAGG CATTGCGCTT GATAAGTTTG ATGAGATTAT 19860

TGGTCGCTTC CAGTTTGGCG TTAGAATAGT GTAGTTGAAG GGCGTTGATA ATCTTTTCTT 19920

TATCTTTGAG GAAGGTTTTA AAGACAGTCT GAAAAATAGG ATGAACCTGC TTAAGATTGT 19980

CCTCAATAAG TCCGAAAAAT TTCTCTGGTT CCTTATTCTG GAAGTGAAAA AGCAAGAGTT 20040

GATAGAGCTG ATAGTGGTGT TTCAAGTCTT CCGAATAGCT CAAAAGCTTG TTTAAAATCT 20100

CTTTATTGGT TAAGTGCATA CGAAAAATAG GACGATAAAA TCGCTTATCA CTCAGTTTAC 20160

GGCTATCCTG TTGAATGAGT TTCCAGTAGC GCTTGATAG 20199

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19702 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ACCCGATGTA TCAGCGGATA TTTACTCTAT TTTTCAAACG ATGTTATACC CACAATAAAA 60

GAAAAAAGAC CCTAAGGTCT CCTTTGCTTT TATTATTAAA CGCGTTCAAC TTTACCTGAT 120

TTCAAAGCAC GAGCTGAAGC CCAAACTTTT TTAGGTTTAC CATCGATAAG AACAGTAACT 180

TTTTGAAGGT TTGGTTTTAC GGCACGTTTT GTTTGGTTCA TCGCGTGTGA ACGGTTGTTT 240

CCTGATACAG TCTTACGACC TGTAAAGTAA CATACTTTAG CCATTGTGTT TTCCTCCTAT 300

TAGATCTAAT ATAGCGGATG TGCTAGCACC ACATACCGTA CTATGTTATC ACATTTTCTT 360

GTTTTTTGCA AGGGAATTGG AAGATTTTTT ATTTGTGTCT TAAATCAGGT CTTGCGTGAC 420

ATTTcTGCTC TCCACATGCC ATCGTTGATT AACAGAACAC CAGAATTAAA ATTATGTGTA 480

TAAAAATCAT CTCTAACTGC AGCTAAGGGT ATAGCCGTCA AGTCCAAATC CCACAGCTCA 540

```
TCTATCGATT TTCTTACAAC AATATCTGAA TCCAAATACA GTACACGAGA CTCGCTTACA    600
TACTTTGGAA TAAAATACCT AAAAAAGCCG CATATGAAAG TCCCTCAAAG GGGAGACGAT    660
AACCTTTCAG AATATTACTG TCAATCTAAA CATTCACAAT CTCACTATTC AAAGTCTCTA    720
GTCTTTTTTC CATCAATTGG AACCATTCTC GCGGAAGGTC ATCATTAAAA ACATAAAACT    780
TAAGATTATA ATGATGAACA CAAAGAGATT TTATTGTTGT TTCAACTTTA TCCATATAAG    840
CATTATCTGC ACCTAAGACA ATCGCTTTTT TCTCTTCTTT CACTTTTTAT CTCATTTCTT    900
TTTATTCCCA TCATATTATT CCCATCATAT GTTTCCCATC ATATGTTTCT ACGTAACCAT    960
TATTTTCGCC TATTCGTTCG TAAAACCATA CCAGTGGAGA TTTTAGATGA AGTCCCATTA   1020
CGGTTTACAA TTTTTACATT ACGACACGGA GTTTTACAAA TCGATTTCAT TTGCCAAACG   1080
TAGTTAGTGA GGCAGTTAGC TAGTTCGCCA AATAGCGACT AGCGTCCAAC AATTTGGAAC   1140
TTTAGTTCCA ATTGTTGGTA CTGAGTCACA TCTTCTCCTC TAACTCTACG TCTGGATACT   1200
TGTCCGCAAA CCAGCGGAGG GCAAAGTCAT TTTCAAAGAG AAAGACTGGT TGGTCAAAAC   1260
GGTCTTTGGC TAAGATATTG CGACTTGACG ACATCCGTTC ATCCAAGTCC TCAGGCTTGA   1320
TCCAACGAAC GGTCTTTTTA CCCATTGGGT TCATAACTAC TTCCGCATTG TACTCGCCTT   1380
CCATGCGGTG TTTAAAGACT TCAAACTGGA GTTGACCTAC AGCGCCTAGC ATGTACTCAC   1440
CTGTTTGGTA ATTCTTATAA AGCTGAACGG CTCCTTCTTG CACCAATTGC TCAATCCCCT   1500
TGTGGAAGGA TTTTTGCTTC ATAACATTCT TAGCAGAAAC TTTCATGAAA ATCTCAGGTG   1560
TAAAGGTTGG CAGGGGTTCA AATTCAAACT TGTTTTTTCC AACCGTCAAG GTATCCCCAA   1620
CCTGATAAGT ACCGGTATCG TAAACCCCGA TAATATCACC TGCCACGGCA TTGGTCACAT   1680
TCTCACGACT CTCCGCCATA AACTGGGTAA CATTAGATAG TTTAGCCCCC TTACCAGTAC   1740
GAGGGAGATT GACACTCATG CCGCGCTCAA ATTCGCCAGA TACGATACGG ACAAAGGCAA   1800
TACGGTCACG GTGACGAGGG TCCATGTTGG CTTGGATTTT AAAGACAAAG CCTGAGAAAT   1860
CCTTGTCATA AGGATCCACA ATTTCACCGT CTGTTTTCTT GTGACCATGT GGTTCTGGAG   1920
CAAACTTGAG GAAGGTTTCA AGGAAGGTCT GCACACCAAA GTTTGTCAGG GCTGAACCGA   1980
AAAAGACAGG CGTCAATTCT CCAGCCAGAA TAGCTTCCTC TGAAAACTCA TTCCCGGCTT   2040
CATTTAAAAG CTCAATGTCA TCCTTGACTT GCTCGTAGAA AGGATTGCTA CCAAAGAGTT   2100
TGTCCCCGTC TTCTAGACTG GCAAAACGCT CATCCCCTTT GTAAAGCTCT AAACGTTGGT   2160
TATAGAGGTC ATACAAGCCC TCAAAGGCTT TCCCCATCCC GATAGGCCAG TTCATAGGGT   2220
AGCTAGCAAT GCCCAAGATT TCTTCCAATT CTTGCAAGAG ATCCAAAGGC TCACGACCGT   2280
```

CACGGTCCAG CTTGTTCATA AAGGTAAAGA CTGGAATGCC ACGATGTTTC ACAACCTCAA 2340

ACAATTTCTT GGTTTGAGCC TCGATCCCCT TGGCAGAGTC CACGACCATG ACCGCAGCAT 2400

CCACCGCCAT CAAGGTACGA TAGGTATCTT CTGAGAAGTC CTCGTGCCCT GGCGTGTCTA 2460

AGATATTCAC GCGCTTGCCG TCGTAGTCAA ATTGCATAAC AGATGAAGTA ACAGAAATCC 2520

CACGTTGCTT CTCGATATCC ATCCAGTCAG ATTTAGCAAA AGTCCCTGTT TTCTTCCCTT 2580

TTACCGTACC AGCCTCACGA ATCTCACCCC CAAAGTAGAG TAACTGCTCA GTGATGGTTG 2640

TTTTCCCCGC GTCCGGGTGG GAGATAATGG CAAAGGTACG ACGTTTCTTA ATTTCTTCTT 2700

GAATATTCAT AAGTTCTCTT TCTTTGATTC TCTATTTTTC TTGTTTCAAT AGCTGAGAAT 2760

GATTTTTACA TTGGATTTTA CCATTCCTTT CAACACTCCA TTATATCGGA TTTTAGCATT 2820

TTTTTCAATT TCTATTTCTT TTCACTTCCC CCTCCCTTAT TTATAGGAAA ATATGGTAAA 2880

ATAGAACAGA CTAAAAATCA TCATTTCACG AAAGGATGCA AGATGAAAAT TACGCAAGAA 2940

GAGGTAACAC ACGTTGCCAA TCTTTCAAAA TTAAGATTCT CTGAAGAAGA AACTGCTGCC 3000

TTTGCGACCA CCTTGTCTAA GATTGTTGAC ATGGTTGAAT TGCTGGGCGA AGTTGACACA 3060

ACTGGTGTCG CACCTACTAC GACTATGGCT GACCGCAAGA CTGTACTCCG CCCTGATGTG 3120

GCCGAAGAAG GAATAGACCG TGATCGCTTG TTTAAAAACG TACCTGAAAA AGACAACTAC 3180

TATATCAAGG TGCCAGCTAT CCTAGACAAT GGAGGAGATG CCTAATGACT TTTAACAATA 3240

AAACTATTGA AGAGTTGCAC AATCTCCTTG TCTCTAAGGA AATTTCTGCA ACAGAATTGA 3300

CCCAAGCAAC ACTTGAAAAT ATCAAGTCTC GTGAGGAAGC CCTCAATTCA TTTGTCACCA 3360

TCGCTGAGGA GCAAGCTCTT GTTCAAGCTA AAGCCATTGA TGAAGCTGGA ATTGATGCTG 3420

ACAATGTCCT TTCAGGAATT CCACTTGCTG TTAAGGATAA CATCTCTACA GACGGTATTC 3480

TCACAACTGC TGCCTCAAAA ATGCTCTACA ACTATGAGCC AATCTTTGAT GCGACAGCTG 3540

TTGCCAATGC AAAAACCAAG GGCATGATTG TCGTTGGAAA GACCAACATG GACGAATTTG 3600

CTATGGGTGG TTCAGGTGAA ACTTCACACT ACGGAGCAAC TAAAAACGCT TGGAACCACA 3660

GCAAGGTTCC TGGTGGGTCA TCAAGTGGTT CTGCCGCAGC TGTAGCCTCA GGACAAGTTC 3720

GCTTGTCACT TGGTTCTGAT ACTGGTGGTT CCATCCGCCA ACCTGCTGCC TTCAACGGAA 3780

TCGTTGGTCT CAAACCAACC TACGGAACAG TTTCACGTTT CGGTCTCATT GCCTTTGGTA 3840

GCTCATTAGA CCAGATTGGA CCTTTTGCTC CTACTGTTAA GGAAAATGCC CTCTTGCTCA 3900

ACGCTATTGC CAGCGAAGAT GCTAAAGACT CTACTTCTGC TCCTGTCCGC ATCGCCGACT 3960

TTACTTCAAA AATCGGCCAA GACATCAAGG GTATGAAAAT CGCTTTGCCT AAGGAATACC 4020

TAGGCGAAGG AATTGATCCA GAGGTTAAGG AAACAATCTT AAACGCGGCC AAACACTTTG 4080

AAAAATTGGG TGCTATCGTC GAAGAAGTCA GCCTTCCTCA CTCTAAATAC GGTGTTGCCG 4140
TTTATTACAT CATCGCTTCA TCAGAAGCTT CATCAAACTT GCAACGCTTC GACGGTATCC 4200
GTTACGGCTA TCGCGCAGAA GATGCAACCA ACCTTGATGA AATCTATGTA AACAGCCGAA 4260
GCCAAGGTTT TGGTGAAGAG GTAAAACGTC GTATCATGCT GGGTACTTTC AGTCTTTCAT 4320
CAGGTTACTA TGATGCCTAC TACAAAAAGG CTGGTCAAGT CCGTACCCTC ATCATTCAAG 4380
ATTTCGAAAA AGTCTTCGCG GATTACGATT TGATTTTGGG TCCAACTGCT CCAAGTGTTG 4440
CCTATGACTT GGATTCTCTC AACCATGACC CAGTTGCCAT GTACTTAGCC GACCTATTGA 4500
CCATACCTGT AAACTTGGCA GGACTGCCTG GAATTTCGAT TCCTGCTGGA TTCTCTCAAG 4560
GTCTACCTGT CGGACTCCAA TTGATTGGTC CCAAGTACTC TGAGGAAACC ATTTACCAAG 4620
CTGCTGCTGC TTTTGAAGCA ACAACAGACT ACCACAAACA ACAACCCGTG ATTTTTGGAG 4680
GTGACAACTA ATGAACTTTG AAACAGTCAT CGGACTTGAA GTCCACGTAG AGCTCAACAC 4740
CAATTCAAAA ATCTTCTCAC CTACTTCTGC CCACTTTGGA AATGACCAAA ATGCCAACAC 4800
TAACGTGATT GACTGGTCTT TCCCAGGAGT TCTACCAGTT CTCAATAAAG GGGTTGTTGA 4860
TGCCGGTATC AAGGCTGCTC TTGCCCTCAA CATGGACATC CACAAAAAGA TGCACTTTGA 4920
CCGCAAGAAC TACTTCTATC CTGATAACCC CAAAGCCTAC CAAATTTCTC AGTTTGATGA 4980
ACCAATCGGA TATAATGGCT GGATTGAAGT CAAACTAGAA GACGGTACGA CCAAGAAAAT 5040
CGGTATCGAA CGTGCCCACC TAGAGGAAGA CGCTGGTAAA AACACCCATG GTACAGATGG 5100
CTACTCTTAT GTTGACCTCA ACCGCCAAGG GGTTCCCTTG ATTGAGATTG TATCTGAGGC 5160
AGATATGCGT TCTCCTGAAG AAGCCTATGC TTATCTGACA GCCCTCAAGG AAGTTATCCA 5220
GTACGCTGGC ATTTCTGACG TTAAGATGGA GGAAGGTTCG ATGCGTGTGG ATGCCAACAT 5280
CTCCCTTCGT CCTTATGGTC AAGAGAAATT CGGTACCAAG ACTGAATTGA AGAACCTCAA 5340
CTCCTTCTCA AACGTTCGTA AAGGTCTTGA ATACGAAGTC CAACGCCAGG CTGAAATTCT 5400
TCGCTCAGGT GGTCAAATCC GCCAAGAAAC ACGCCGTTAC GATGAAGCGA ATAAAGCAAC 5460
CATCCTCATG CGTGTCAAGG AAGGGGCTGC TGACTACCGC TACTTCCCAG AACCAGACCT 5520
ACCCCTCTTT GAAATTTCTG ACGAGTGGAT TGAGGAAATG CGGACTGAGT TGCCAGAGTT 5580
TCCAAAAGAA CGTCGTGCGC GTTATGTATC TGACCTTGGT TTATCAGACT ACGATGCTAG 5640
TCAGTTGACT GCTAATAAAG TCACTTCTGA CTTCTTTGAA AAAGCTGTTG CCCTAGGTGG 5700
TGATGCCAAA CAAGTCTCTA ACTGGCTCCA AGGGGAAGTC GCTCAGTTCT TGAATGCTGA 5760
AGGTAAAACA CTGGAACAAA TCGAATTGAC ACCAGAAAAC TTGGTTGAAA TGATTGCCAT 5820

CATCGAAGAC GGTACTATTT CATCTAAGAT TGCCAAGAAA GTCTTTGTCC ATCTAGCTAA 5880

AAATGGCGGT GGCGCGCGTG AATACGTGGA AAAAGCAGGT ATGGTTCAAA TTTCAGATCC 5940

AGCTATCTTG ATCCCAATCA TCCACCAAGT CTTTGCCGAT AACGAAGCTG CTGTTGCCGA 6000

CTTCAAGTCA GGCAAACGTA ACGCCGACAA GGCtTTACAG GATTCCTTAT GAAGGCAACC 6060

AAAGGCCAAG CCAACCCACA AGTTGCCCTT AAACTACTTG CACAGGAATT GGCGAAGTTG 6120

AAAGAAAACT AGACAGAACA AAACCAGCCC TAAGGTTGGT TTTTTCTTCT CTACCAACTC 6180

CCAATAACTA TTTTGGCTTT ATTTCCAGAG TATTTTATGG TAAAATGAAG AGTAATAATA 6240

TTTATTAAAG AGGTAAAAAC ATGATTGAAG CAAGTACCTT AAAAGCTGGT ATGACCTTTG 6300

AAACAGCTGA CGGCAAATTG ATTCGCGTTT TGGAAGCTAG TCACCACAAA CCAGGTAAAG 6360

GAAACACGAT CATGCGTATG AAATTGCGTG ATGTCCGTAC TGGTTCTACA TTTGACACAA 6420

GCTACCGTCC AGAGGAAAAA TTTGAACAAG CTATTATCGA GACTGTCCCA GCTCAATACT 6480

TGTACAAAAT GGATGACACA GCATACTTCA TGAATACAGA AACTTATGAC CAATACGAAA 6540

TCCCTGTAGT CAATGTTGAA AACGAATTGC TTTACATCCT TGAAAACTCT GATGTGAAAA 6600

TCCAATTCTA CGGAACTGAA GTGATCGGTG TCACCGTTCC TACTACTGTT GAGTTGACAG 6660

TTGCTGAAAC TCAACCATCT ATCAAAGGTG CTACTGTTAC AGGTTCTGGT AAACCAGCAA 6720

CGATGGAAAC TGGACTTGTC GTAAACGTTC CAGACTTCAT CGAAGCAGGA CAAAAACTCG 6780

TTATCAACAC TGCAGAAGGA ACTTACGTTT CTCGTGCCTA ATCTCTAGAA AGAGGTCATT 6840

CTATGGGAAT TGAAGAACAA CTTGGCGAAA TCGTTATCGC CCCACGTGTA CTTGAAAAAA 6900

TCATTGCTAT CGCTACTGCA AAGGTAGAGG GTGTTCACTC TTTTTCAAAC AGATCAGTGT 6960

CTGATACCCT TTCAAAACTT TCACTCGGCC GTGGCATTTA TCTTAAAAAC GTGGACGAAG 7020

AACTCACAGC AGATATCTAT CTCTACCTTG AGTACGGAGT AAAAGTTCCT AAGGTAGCGG 7080

TTGCTATCCA GAAAGCTGTC AAAGATGCCG TCCGTAATAT GGCTGATGTA GAACTCGCTG 7140

CTATCAATAT TCACGTTGCA GGTATCGTCC CAGATAAAAC ACCAAAACCA GAATTGAAAG 7200

ATCTATTTGA CGAGGACTTC CTCAATGACT AGTCCACTAT TAGAATCTAG ACGCCAACTC 7260

CGTAAATGCG CTTTTCAAGC TCTCATGAGC CTTGAGTTCG GTACGGATGT CGAAACTGCT 7320

TGTCGTTTCG CCTATACTCA TGATCGTGAA GATACGGATG TACAACTTCC AGCCTTTTTG 7380

ATAGACCTCG TTTCTGGTGT TCAAGCTAAA AAGGAAGAAC TAGATAAGCA AATCACTCAG 7440

CATTTAAAAG CAGGTTGGAC CATTGAACGC TTAACGCTCG TGGAGAGAAA CCTCCTTCGC 7500

TTGGGAGTCT TTGAAATCAC TTCATTTGAC ACTCCTCAGC TGGTTGCTGT TAATGAAGCT 7560

ATCGAGCTTG CAAAGGACTT CTCCGATCAA AAATCTGCCC GTTTTATCAA TGGACTGCTC 7620

AGCCAGTTTG TAACAGAAGA ACAATAAGGC TCTTTGTCAA CTGTAGTGGG TTGAAAAAAA 7680
GCTAAGCTCG AGAAAGGACA AATTTCGTCC TTTCTTTTTT GATGTTCAAA GCGATAAAAA 7740
TCCGTTTTTT GAAGTTTTCA AAGTTTCGAA AACCAAAGGC ATTGCGCTTG ATAAGTTTGA 7800
TGAGATTATT GGTCGCTTCC AGTTTGGCAT TAGAATAGTG TAGTTGAAGG GCGTTGACAA 7860
TCTTTTCTTT ATCTTTGAGG AAGGTTTTAA AGACAGTCTG AAAAATAGGA TGAGCCTGCT 7920
TAAGATTGTC CTCAATAAGT CCGAAAAATT TCTCTGGTTC CTTATTCTGG AAGTGAAACA 7980
GCAAGAGCTG ATAGAGCTGA TAGTGGTGTT TCAAGTCTTG TGAATGGCTC AAAAGCTTGT 8040
CTAAAATCTC TTTATTGGTT AAGTGCATAC GAAAAGTAGG ACGATAAAAT CGCTTATCAC 8100
TCAGTCTACG GCTATCCTGT TGAATGAGTT TCCAGTAGCG CTTGATATCC TTGTATTCAT 8160
GGGATTTTCG ATGAAACTGA TTCATGATTT GGACACGCAC ACGACTCATG GCACGGCTAA 8220
GATGTTGTAC AATGTGAAAG CGATCAAGAA CGATTTTAGC ATTCGGGAGT GAAACAGTCT 8280
GGGAGACTGT TTCAGCCTGA GCCTAGGAAT TTGAAAGCGA AGCTGTTTAG CCAAGTCATA 8340
GTAAGGGCTA AACATATCCA TAGTAATAAT TTTGACGCGA CATCGGACAA CTCTATCGTA 8400
GCGAAGAAAG TGATTTCGAA TGATAGCTTG TGTTCTACCC TCAAGAACAG TGATGATATT 8460
GAGATTGTTA AAATCTTGCG CAATGAAGCT CATCTTTCCC TTTGTAAAAG CATACTCATC 8520
CCAAGACATA ATCTCAGGAA GACAAGAAAA ATCATGTTTA AAGTGAAAAT CATTGAGCTT 8580
ACGAATAACA GTTGAAGTTG AGATGGAAAG CTGATGGGCA ATATCAGTCA TAGAAATCTT 8640
TTCAATCAAC TTTTGAGCAA TCTTTTGGTT GATGATACGA GGGATTTGGT GATTTTTCTT 8700
GACGATAGAA GTTTCAGCGA CCATCATTTT TGAACAGTGA TAGCACTTGA ATCGACGCTT 8760
TCTAAGGAGA ATTCTAGTAG GCATACCAGT CGTTTCAAGA TAAGGAATTT TAGAAGGTTT 8820
TTGAAAGTCA TATTTCTTCA ATTGGTTTCC GCACTCAGGG CAAGATGGGG CGTCGTAGTC 8880
CAGTTTGGCG ATGATTTCCT TGTGTGTATC CTTATTGATG ATGTCTAAAA TCTGGATATT 8940
AGGGTCTTTA ATGTCTAGTA ATTTTGTGAT AAAATGTAAT TGTTCCATAT GAATCTTTCT 9000
AATGAGTTGT TTTGTCGCTT TTCATTATAG GTCATATGGG ACTTTTTTTC TACAATAAAA 9060
TAGGCTCCAT AATATCTATA GGGGATTTAC CCACTACAAA TATTATAGAG CCAACAATAA 9120
AAAGAAAAAG TGTTTGATAG ATATCAAACA CTTTTTTCTT TGCCTCCCAC TATCTAAAAA 9180
AATGATAATA GATATAATTG TAAACAAAAA TCCAGATAGG TTTTGCATGA TTGAGAAAGT 9240
TAAAAAAACT ATGGCAGAGA ATCGTTAATC TCAGATTGTC GGTAGAACGA TAAACAAGGG 9300
CAAAAAAGAA ACCAATCAGA CTATAATATA ATAAACTAAT TGGATCTCTG TGAGATAGTA 9360

TCAAATGGCT AATCCCAAAG ATGATAGCAG ATAGGATAAC ATCCAAATAG TACTTGGACT 9420

AGGGAAAGAA GGTATTCATA AAATACCCTC TATCAAGAGT CTCCTCAAAA ACAGGACCGA 9480

TGATTACAGG CAGGACAAAA GATAAGATAG TCGATAAAAA GGTTGGTTGT CCATTTGAAA 9540

AAAGCACGGT AAAATACTCA TCATGAATAT TCCTATGATT AATCAAATGA GCATAGCGTG 9600

CCCAAAAATT ACCGAGAATC TGATAAACCA CATAAGTTGC AAATAAGTAG AAGACAAATG 9660

ACCAGTTCCA GCTCTTTTTC TCAAAGATAA AGAGCATCTT TTTCTTTTTT AACCTCCAAA 9720

TTAATAGAAG GAAACTTCCC ACTAATCCCA TTGTTAAAAT AAGAGAATAG ACATCAGCTC 9780

CTAACCCTAA AATGATCGTC ACATACAATC CAATTGTTTG TGGTAAATAG GTAGATAGTA 9840

AAATAATAAG CAAAAATATT CCAAATTGTC TTAGTTTTTT TGTGTTTCTC ATCGTACTTT 9900

TTTGAAAGAT TACCCTGCTC GGAAGCCGTA CTTCCAAGCA TCTATATAAG AATTAAGTGC 9960

CCCTTGCCTC ATATAGGGAG CAAATTCTCT ATAATATAAC CATCTACTAT ATCCATCTTC 10020

CCAAACAGCA AGACCACCTG AAGTTTGCTC CAAGTCCTCA GTTGAAAGAA CTGTAAATGT 10080

ATTTGTACCT GTCATTGCAA GTACCTTCTT AAAATAGATT GTTGTAGGCT CACATTTATA 10140

GTATATTTCT TTTTTTGTCT ATTTTATAGC CCATCTCCTC AACTGGCAAT TTTTCGACCT 10200

GAATTACATT TTTCCATAAA AAATGAGACC TTTCTAGTCT CATTTAGTCA TTCTTAGTAT 10260

TTTCTAAATC GTTGATAGCG TTCTTCCAGC AACTCTTCTA GCGGTTTTTG TGAAAGTCTA 10320

GCCAGCTCCG TTTGGAGTTC TTTTTTGACA CTCTTAATCA GTTCTTTACT AGAAAGTCCT 10380

ATTTCAGAAA TCACCTTATC CACCACGTCC ATTTCTAACA GTTCATGCGA AGTGATTTTC 10440

ATCAGTTCTG CTGCTTCCAT AGCGCGAGTA CCGTCCTTCC ATAAAATGGA AGCAAAGCCT 10500

TCTGGACTGA GAATGGCATA GATAGAATTT TCCAGCATCC AGACACGGTC CGCGACAGCT 10560

AGAGCCAGAG CCCCGCCTGA ACCACCTTCA CCGATAATAA TGGCGATAAT AGGAACTTTC 10620

AGGTCACTCA TTTCCATGAG ATTGCGAGCG ATAGCTTCCC CTTGACCACG TTCTTCCGCT 10680

CCGACACCAG GATAAGCACC TGCTGTATTG ATAAAGGTCA CAACTGGACG GCCAAATTTC 10740

TCAGCCTGTT TCATCAACCG CAGTGCCTTT CGGTAGCCTT CTGGATGTGG TTGGCCAAAA 10800

TTCCGTTTGA GGTTGTCTTG CAAACTCTTG CCTTTTTGGA TACCAACCAC TGTTACAGCT 10860

TGGTCTCCAA GCCAACCAAT ACCACCAACA ACTGCACCAT CATCACGAAA AGAACGGTCA 10920

CCATGTAATT GGATAAATTC ATCAAAAATG CCTGTCGCAA AGTCCAAGGT TGTCAAGCGA 10980

CTCTGCTCAC GCGCTTCTCT GACTATTTTT GCAATATTCA TCTAGGACTC CCTCCATGCA 11040

ATCTGACTAG GCTAGCAATC GTATCTGGTA AGTCTCTTCT TTTGACAATA GCATCCACAA 11100

AGCCATGTTC TAATAGGAAT TCTGCCTTTT GGAAATCCTC AGGCAAGCTT TCACGAACCG 11160

TATTTTCAAT CACACGACGC CCAGCAAAAC CAACCAAGCT CTGTGGTTCA GCCAGAATGA 11220
TATCGCCTTC CATAGCGAAA GAAGCTGTCA CACCACCAGT CGTTGGATCT GTCAAAATGG 11280
TCAGGTAAAA GAGACCAGCA TTTGAATGGC GTTTAACCGC CGCAGAGATC TTAGCCATCT 11340
GCATGAGACT CATGATTCCT TCCTGCATAC GGGCTCCACC AGAGGCTGTG AATAGGACAA 11400
CTGGCAATTT TTCGACAGTC GCATACTCAA ACAAACGAGT GATTTTTTCA CCTACAACCG 11460
TACCCATAGA AGCCATGATA AAGTTAGAAT CCATAATCCC AAGAGCCACA GTCTGACCTT 11520
TAATAAGAGC AGTTCCTGTC ACAACGGCTT CATGCAGACC TGTTTTTTCA CGCATAGATG 11580
CCAGTTTCTT TTGGTAACCA GGGAAATGCA AGGGATCCTT GCTTTCAATC CCTGTAAACA 11640
ATTCTTTGAA GGTTCCCATA TCAATCGTCA AAGCCAAGCG TTCTTGGGCA GAAATACGAA 11700
AGGTATAGCT ACAGTGCGGA CAGATACGTT CACTTCCCAG ATCCTTCTGA TAGATGGTAT 11760
GCTTACAGCC TGGACACTGG GAAAATAATT CATCTGGAAC CTCTGGCTTA GCTTGAGGTT 11820
TTTCCCTAAC CGAACGATTG GGATTGATTC GAATATACTT ATCTTTTTTA CTAAATAGAG 11880
CCATTGATTC CCCTTTTCGG TTTAAACTCT TAAAGTCATT TTATTCTTTT TCTTGATATT 11940
TAGGTAAGAA GGTTTCCATC AAGAAGGAAG TATCATAATC CCCAGCAATG ACATTGCGAT 12000
CTGAAATGAG GTCAAGCTGG AAATCTGCAT TGGTCTGCAC TCCTTCAATT TCTAATTCAT 12060
AGAGGGCACG TTGCATTTTC ATCAAGGCGT CAAAACGATT TTCGCCGTGT ACTATGATTT 12120
TGGCAATCAT ACTATCATAA TAAGGCGGAA TGGTATAACC TGGATAAACT GCTGAATCCA 12180
CGCGCAAGCC AACTCCACCA CTTGGCAGAT AGAGATTAGT AATCTTACCT GGACTTGGAG 12240
CAAAGTTAAA GGCTGGGTTT TCTGCATTGA TACGACACTC GATGGCATGA CCGCGTAGGA 12300
CAATATCTTC TTGCTTAACA GACAAAGGCT GACCTGCCGC AATGCAAATC TGTTCCTTAA 12360
CGATATCAAC ACCTGAAACA AACTCTGTTA CTGGATGTTC TACCTGAACA CGAGTATTCA 12420
TCTCCATGAA ATAGAAATTG CTACTTGCTT CATCAAGAAG AAATTCAATG GTTCCTGCAT 12480
TCTCATAGCC AACAAACTCT GCCGCTCGAA CAGCAGCAGC ACCTATTTCA TGACGCAGCG 12540
TTTTTCCGAT TGCAATCGAG GGACTTTCTT CCAAAACCTT TTGGTTATTC CTTTGAAGAG 12600
AACAATCCCG TTCACCCAAG TGAATCACAT GTCCATGCTC ATCACCTAGG ATTTGAACCT 12660
CAATGTGCCG AGCTGGATAG ATAACCCGTT CTATGTACAT GGCACCATTG CCATAATTGG 12720
CCTTGGCCTC ACTAGAGGCA GTTTCAAAGG CAGAAACGAG GTCATCTGGT TTTTCAACCT 12780
TACGAATCCC TTTACCACCT CCACCTGCTG AAGCCTTGAG CATAACAGGA TAGCCAATTT 12840
TTTCAGCAAC AATCAAAGCT TCTTCAGAGT TATGCACTTC TCCATCTGAA CCTGGTATAA 12900

CAGGCACACC TGCTTTAATC ATCTGAGCAC GCGCATTGAT CTTATCCCCC ATCATATCCA 12960
TAACATGACC AGATGGACCG ATAAACTTGA TACCTACTTC TTCACACATG GTCGCAAATT 13020
TGGAATTTTC ACTGAGAAAT CCAAAACCAG GGTGAATAGC TTCTGCCTCA GTCAAGACTG 13080
CAGCTGATAG AACTGCATTA ATATTGAGAT AAGACTCTGT TGCCTTGCCA GGACCAATAC 13140
AAACTGCTTC ATCTGCCAAA AGCGTATGAA GAGCTTCCTT ATCAGCAGTT GAATAAACCG 13200
CTACCGTCGC AATCCCCAAT TCACGTGCCG CACGGATAAT ACGAACCGCA ATTTCACCAC 13260
GATTGGCAAT TAAAATTTTT CGAAACATGG AGAACCTCCT TAGTTCCCAA TTGCAAAAGT 13320
AAGGGTACCA CTGGCTGCAA GCTTGCCATC CACTTCAGCC TTTGCTTCAA CCACAGCTAT 13380
GGTGCCACGA CGTTTTACAA AAGTCGCTGT CATAACCAAT TGGTCGCCTG GTACAACTTG 13440
CTTCTTGAAC TTAACCTTGT CCATACCAGC GTAAAAGACC AGTTTTCCTT TATTTTCAGG 13500
TTTTGATAAC TCCAACACAC CGGCAGTTTG CGCCAAGGCT TCCATAATCA CAACACCTGG 13560
CATAACTGGG TATTGAGGAA AGTGGCCGTT AAAGAAAGGC TCGTTGATGG TCACATTTTT 13620
GATAGCAACA ATGGTATCCT CGCTCACTTC CAAGACACGG TCCACTAGAA GCATAGGATA 13680
ACGGTGGGGA AGAGCTTCTT TGATTCCTTG AATATCGATC ATTTGATACG TACCAATCCT 13740
TTACCAAACT CAACCATTTC TTCGTTAGAG ACGAGAATTT CCGTTACCAC ACCATCCTTA 13800
GGAGCTGGGA TTTCATTCAT GACTTTCATG GCTTCGATAA TTACCAATGT TTGACCTTTT 13860
TTGACACTAT CACCAACTGT AACGAAGGCA GGTTTATCTG GTCCAGCAGC CAAGTAAACC 13920
ACTCCAACAA GTGGACTCTC TACAAGATTT CCCTCAGTAG CCACACTTGC TTCAGCTGGA 13980
GCTGGAACTT CTTCTGCTAC AGTCTCTGCT GGAGCAGATG TAGGAGCTAC TGGACTCGGT 14040
GTTGCTAGAA CGGGTGCTGG AGCGACTTGA GTTGCAACTT CAGGCACAGG TCTTGCTTCA 14100
TTCTTGCTAA ACTGCAACTC ATCCGTCCCA TTTTTATAAG AAAATTCTCT CAAACTTGAC 14160
TGGTCAAATT GAGTCATCAA GTCTTTAATA TCGTTTAAAT TCATACTTAT CTATTCTCCC 14220
AACGTTTGAA AGCAAGAACT GCATTGTGGC CTCCAAAACC AAAAGTATTT GAAATAGCGT 14280
ATGGAATTTC TTTCTCCAAG CCTTGTCCAT AAACGACATT AGCTTCGATA TAATCTGATA 14340
CTTCACTTGT CCCAGCTGTC ATTGGTACAA AGTTATGACG CATAGCTTCG ATGGTGACGA 14400
TAGCTTCTAC TGCACCCGCA GCCCCCAGCA AATGTCCTGT AAAAGACTTG GTTGATGATA 14460
CAGGTACTTC CTTACCAAGA ACAGCTACGA TAGCACCACT TTCTCCTTTT TCATTGGCAG 14520
GAGTTGACGT TCCGTGAGCA TTGACATAGG CTACTTGCTC TGGAGAAATC TCAGCTTCTT 14580
CCAAGGCTAG TTTGATGGCC TTGATAGCTC CCTGACCTTC TGGATGTGGA GAAGTCATGT 14640
GGTAGGCATC ACAAGTATTT CCGTAACCAA CCACTTCAGC CAGGATAGTA GCTCCACGTT 14700

TTTCAGCGTG TTCAAGACTT TCTAGAACCA ACATCCCTGA ACCTTCACCC ATAACAAACC 14760

CATTGCGATC CTTATCAAAT GGGATCGAAG CACGAGTTGG ATCCTCTGTA GTAGAGAGAG 14820

CTGTTAAGGC TTGGAAACCA GCGATGGCAA AAGGTGTGAT AGAAGCTTCT GTTCCTCCCA 14880

CCAACATCAC ATCTTGGAAA CCAAACTTAA TGGAGCGGAA GGCATCCCCA ATCGCATCAT 14940

TTGATGAAGA GCAGGCAGTA TTGATAGATT TACAAACACC GTTTGCACCA AAACGCATGG 15000

CTACATTCCC AGAAGCCATA TTTGGTAAAG CTTTTGGAAG AGTCATTGGT TTGACACGTT 15060

TGGGTCCTTT TTCATGAAGG CGAAGTACCT GATCTTCAAT TTCCTTGATT CCACCAATAC 15120

CAGATGCAAC GATAACACCA AAACGATCCC TATTAAGAGC CTCTACATCA AGATTGGCAT 15180

GATTTACAGC CTCTTGGGCT GCATACAAGG CATATAAAGA ATAGTTATCA AAACGGTTGG 15240

TATCTTTTTT TACAAAGTAT TTATCGAACG GAAAATCTTG GATTTCTGCC GCATTATGCA 15300

CATCAAAGTC ACTATGATCA AATTTTGTAA TGCCACCAAT GCCGATTTTC CCAGTTGCTA 15360

AACTATTCCA AAATTCTTCT GGTGTATTTC CGATTGGAGA TGTTACTCCA TAACCTGTTA 15420

CCACTACTCG ATTTAGTTTC ATTCTTTTCA CCTCTAGCTT TCGCTACATA CTTAAGCCAC 15480

CATCAATGGC AACCACTTGT CCAGTTAGAT AATCTTGGCC TGCTAAAAAT ACTGTCAAAT 15540

CTGCAACCTG CTCTGCCTGC CCAAATTCTT TCATCGGAAT CTGAGCTAGT GTAGCTTCCT 15600

TAATCTTATC TGACAGGATA GCGGTCATAT CAGACTCAAT CATTCCTGGA GCAATCACAT 15660

TGACTCGTAT ATTCCGACTA GCGACCTCGC GTGCCACAGA CTTGGTAAAG CCAATCAAGC 15720

CAGCCTTAGA AGCAGCATAA TTAGCTTGAC CAATATTCCC CATCAAACCA ACAACACTAG 15780

ACATATTAAT GATAGCACCT TCTCTGGCTT TCATCATCGG TTTCAAGACT GATTGTGTCA 15840

TATTAAAGGC ACCAGTCAGA TTGACCTTGA GCACTTTTTC AAAATCTGCT TCTGTCATCT 15900

TGAGCATAAG AGTATCTTGG GTAATCCCTG CATTGTTGAC CAAAACATCT ACTGAACCCA 15960

GTTCTGCAAT AGCTTGATCA ATCATACGCT TAGCGTCTGC AAAATCTGAT ACATCTCCTG 16020

AAATGGGAAC CACCTTGATA CCATAGTTTG AAAACTCAGC GAGCAATTCT TCTGAGATTG 16080

CCCCACGACT GTTTAAGACA ATGTTGGCTC CTGCTTGAGC AAACTTGTGG GCGATGGCAA 16140

GACCAATTCC ACGACTCGAA CCTGTAATAA AGATATTTTT ATGTTCTAGT TTCATTTTTT 16200

TCCTTTCAAA ACTTCTACTT ATTTTAGTCT ATTTTTCTAA AAGTGCTACT AAACTCGCTT 16260

GATCTTCCAC ATGAGCTAAG TGAGCAGTTT GATCAATTTT TTTAACAAAA CCTGACAAGA 16320

CTTTCCCCGG TCCAATCTCG ATAAAGTTGC TTATGCCTGC TTCTTGCATG ACCCCAATAC 16380

TTTCATAGAA ACGAACGGGT TCCTTGACCT GACGCGTCAA GAGCTGAGCA ATGTCCTCTT 16440

```
TTTGCATCAC AGCAGCTTCT GTATTGCCGA CTAGGGGACA AGTAAAATCT GAAAAACTTA   16500
CCTGAGCTAG AGTTTCAGCT AGTTTCTGGC TAGCAGGTTC AAGGAGAGCG GTGTGAAAGG   16560
GACCTGACAC CTTAAGAGGA ATCAAGCGTT TGGCACCTGC TTCTTGCAAA AGTTCAACCG   16620
CTCGATCAAC TGCAACCACT TCTCCAGCAA TGACGATTTG TGCAGGTGTG TTATAGTTGG   16680
CTGGAGTAAC CACTCCAAGT TCAGAAGCTT TTTGACAGGC TTCTTCAATG ACCTCTACTG   16740
GCGTATTGAG AACTGCTACC ATCTTGCCAG AGTCAGCAGG AGCCGCTTCT TCCATATAGG   16800
CTCCACGCTT AGCTACCAAG GCAACCGCAT CTTCAAAATC CAAGGCGCCA CTTGCCACCA   16860
AGGCAGAGTA TTCTCCAAGA GACAAACCAG CAACCATATC AGGCTGATAG CCCTTTTCTT   16920
GCAATAAACG GTAGATAGCA ACCGAAGTCG CTAGAATGGC TGGTTGCGTA TAGCGGGTCT   16980
GATTGAGTTT GTCTTCTTCC GTATCGATGA GATAACGCAA ATCATAACCG AGCACCTGGC   17040
TCGCTCGATC AATCGTTTCT TTAACAATCG GATACTGATC ATAGAAATCC CGTCCCATCC   17100
CTAGATACTG GGCACCTTGA CCAGCAAATA AAAAGGCTGT TTTAGTCATT TCTTACAACT   17160
CCTGTCCAGC GAGAGGCTTC TTCTTGAATT TTCTTAGCGG CTCCGTAATA CAAATCTTTT   17220
AGGATTTCTT CAGCTGTTTC TTCTTTAGAA ACAAGCCCTG CGATTTGACC TGCCATAACA   17280
GAGCCACCAT CCACATCACC GTGAACAACT GCTTTGGCTA GAGCACCTGC TCCCATTTGT   17340
TCAAAGATTT CTAAATCAGG ATCTTCTTGC TTAAAGGCAT CTTTTTCAGC CAGTTCAAAA   17400
TCTCTAGTCA ACTGATTTTT AATAGCACGA ACAGCATGAC CAAAGTGCTG AGCTGAAATC   17460
GTAGTATCAA TATCCCTTGC TTTTAAAATT TTCTCCTTGT AGTTTGGATG GGCATTCGAC   17520
TCTTTTGCAA CTACAAACCG TGTCCCCACC TGTACAGCCT CTGCACCTAG CATAAAGCCA   17580
GCCGCAGCAC CTTCACCATC CGCAATTCCT CCTGCAGCAA TAACAGGAAT AGATATAGCT   17640
GTGGCTACCT GTCGCACCAA GGTCATGGTT GTTAATTTAC CGATATGCCC CCCAGCTTCC   17700
ATTCCTTCTG CAATAACAGC GTCTGCACCG ATTTTTTCCA TGCGTTTAGC TAAAGCGACA   17760
CTAGGAACAA CAGGAATAAC GATTATCCCA GCTTCATGGA AACGTTCCAT ATACTTGCTT   17820
GGATTTCCTG CTCCTGTTGT GACAACTTTA ACACCTTCTT CAATAACGAG ATCCACGATG   17880
TCTTCCACAA AGGGAGATAA GAGCATGATG TTGACCCCAA AGGGTTTATC AGTCAATGAT   17940
TTGATTTTAT CAATATTGGC CTTGACAACT TCTTTCGGGG CATTTCCCCC ACCGATAATT   18000
CCTAATCCTC CAGCCTTGGA AACAGCCCCT GCCAAATCAC CATCAGCAAC CCAGGCCATC   18060
CCTCCTTGGA AAATAGGATA ATCAATCTTC AATAATTCTG TAATACGCGT TTTCATAGTG   18120
CCTCCAACCT TCCTTGCTTA CGTAATAGTT CGATTTCACC ATAATTTGAC AGTCAAACTA   18180
TTACCTAAAC AAGAGGGAGT GGGTTTCTCC CTACTCCTTC TACTAATATT CTGCTTATTT   18240
```

TGCTTGCTCT TCAACGTAAG CAACCAAGTC ACCAACTGTT TTCAAGTCAT TTTCTGCTTC 18300

GATTTGGATA TCAAAAGCAT CTTCGATTTC TGAGATTACT TGGAACAAGT CCAATGAATC 18360

TGCGTCCAAA TCATCAAAAG TTGATTCAAG TGTTACTTCT GATGCGTCTT TTCCAAGTTC 18420

TTCAACGATA ATTTCTTGTA CTTTTTCAAA TACTGCCATG ATAGGACTCC TTTAAAATAA 18480

ATAGTTTTTT TATAACAATG TGTTCACCAC ATGATTACCT AAATTGTAAG AATGAGCGTG 18540

CCCCAGGTCA AGCCTCCACC GAAGCCTGAT AGAAGAACAG TCTGGCTACC ATCTAAAGGG 18600

ATGAGACCTT GTTCTACACA CTCTGAAAGT AAAATCGGGA TACTGGCTGC ACTGGTATTG 18660

CCATATTCCA TCATATTGGC TGGAAGTTTG GCTCGGTCAA CACCAATTTT TCTAGCCATC 18720

TTATCCAAAA TACGGTCATT GGCTTGATGA AGTAGCAGAT AATCCAAGTC TGTCACCTCT 18780

ATAGGAGATT CATCAATAGT CTGCTTGATA GACTTGGCTA CATCTCGAAT GGCAAAATCA 18840

AAGACTGTGC GTCCATCCAT CTTCAAAAAC GAATCTGCAC TTTCTTGATC TGAAAATGGA 18900

GAATGTAAAC CTGAATGCCC ATAAGTTAAA CACTCGCTGC GACTTCCATC GCTATTGAGA 18960

CTCTCAGCTA AGAAATGCTC TTGCTCGCTA GCTTCTAACA AGACACCACC AGCACCATCT 19020

CCAAACAACA CAGCTGTTGA TCGATCCGAC CAATCGACTG CCTTAGAGAG GGTTTCACTA 19080

CCAATCACCA AGCCTTTTTG AAAGCGACCA GAAGCGATAA ACTTTTCAGC AGTTGAAAGA 19140

GCAAATACAA ATCCACTGCA AGCCGCGGTT AAGTCAAAAG CAAAGGCTTT ATTAGCACCA 19200

ATATTAGCTT GAACACGAGC AGCTGTAGAG GGCATCATCG AATCTGGAGT AATGGTAGCT 19260

AGGATGATAA AATCCAGTTC TTCTCCTGTT ATTCCAGCTT TTGCCATCAG TTTCTTAGCA 19320

ACCTCTGTAG CCAAATCACT GGTAGATTCT GTTCTTGAAA TATGCCTTTG TCGTATTCCC 19380

GTTCGACTTG AAATCCACTC ATCATTGGTA TCCATAATCT GAGCCAAGTC GTGATTTGTA 19440

ACCACTTGCT CTGGCACATA ATGAGCAACC TGACTTATTT TTGCAAAAGC CATTATTTCA 19500

AATCCTCCAA AAATTGGTAA AGATTAGTCA AACCTTTACC CATGACAGCA ATTTCTTCCT 19560

CGCTCATGCC ATCAATAATT TTTTCTACCA TGGCCTTGTG GAAGCGTTTA TGCAGTCTAT 19620

GAATCAAGCG ACCCTTCTTT GTCAAATGCA GATGCACCAC ACGACGATCC TGTTCTGACC 19680

GAACTCGCTC AATGTAGCCC GG 19702

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GAAAATTTCC TCTCTTCTCT TGAAAAATTT TGAAAAAATG GTATGATAGT AACAAGTTAT 60

TTTTAAGAGG AAAGAAAGGG GAATAATGGA GAAAATCAGT TTAGAATCTC CTAAGACGGG 120

GTCGGACCTA GTTTTGGAAA CACTTCGTGA TTTAGGAGTT GATACCATCT TTGGTTATCC 180

TGGTGGTGCG GTTTTGCCTT TTTATGATGC GATATATAAT TTTAAAGGCA TTCGCCACAT 240

TCTAGGGCGC CATGAGCAAG GTTGTTTGCA TGAAGCTGAA GGTTATGCCA AATCAACTGG 300

AAAGTTGGGT GTTGCCGTCG TCACTAGTGG ACCAGGAGCA ACAAATGCCA TTACAGGGAT 360

TGCGGATGCC ATGAGCGATA GCGTTCCCCT TTTGGTCTTT ACAGGTCAGG TGGCGCGAGC 420

AGGGATTGGG AAGGATGCCT TTCAGGAGGC AGACATCGTG GGAATTACCA TGCCAATCAC 480

TAAGTACAAT TACCAAGTTC GTGAGACAGC TGATATTCCG CGTATCATTA CGGAAGCTGT 540

CCATATCGCA ACTACAGGCC GTCCAGGGCC AGTTGTAATT GACCTACCAA AAGACATATC 600

TGCTTTAGAA ACAGACTTCA TTTATTCACC AGAAGTGAAT TTACCAAGTT ATCAGCCGAC 660

TCTTGAGCCG AATGATATGC AAATCAAGAA AATCTTGAAG CAATTGTCCA AGGCTAAAAA 720

GCCAGTCTTG TTAGCTGGTG GTGGAATTAG TTATGCTGAG GCTGCTACGG AACTAAATGA 780

ATTTGCAGAA CGCTATCAAA TTCCAGTGGT AACCAGTCTT TTGGGACAAG GAACGATTGC 840

AACGAGTCAC CCACTCTTTC TTGGAATGGG AGGCATGCAC GGGTCATTCG CAGCAAATAT 900

TGCTATGACG GAAGCGGACT TTATGATTAG TATTGGTTCT CGTTTCGATG ACCGTTTGAC 960

GGGGAATCCT AAGACTTTCG CTAAGAATGC TAAGGTTGCC CACATTGATA TTGACCCAGC 1020

TGAGATTGGC AAGATTATCA GTGCAGACAT TCCTGTAGTT GGAGATGCTA AGAAGGCCTT 1080

GCAAATGTTG CTAGCAGAAC CAACAGTTCA CAACAACACT GAAAAGTGGA TTGAGAAAGT 1140

CACTAAAGAC AAGAATCGTG TTCGTTCTTA TGATAAGAAA GAGCGTGTGG TTCAACCGCA 1200

AGCAGTTATT GAACGAATTG GTGAATTGAC GAATGGAGAT GCCATTGTGG TAACAGACGT 1260

TGGTCAACAC CAAATGTGGA CAGCTCAGTA TTATCCCTAC CAAAATGAAC GTCAGTTAGT 1320

GACTTCAGGT GGTTTGGGAA CAATGGGCTT TGGAATTCCA GCAGCAATCG GTGCTAAAAT 1380

TGCTAACCCA GATAAGGAAG TAGTCTTGTT TGTTGGGGAT GGTGGTTTCC AAATGACCAA 1440

CCAGGAGTTG GCTATTTTGA ATATTTACAA GGTGCCAATC AAGGTGGTTA TGCTGAACAA 1500

TCATTCACTT GGAATGGTTC GCCAGTGGCA GGAATCCTTC TATGAAGGCA GAACATCAGA 1560

GTCGGTCTTT GATACCCTTC CTGATTTCCA ATTGATGGCG CAGGCTTATG GTATTAAAAA 1620

CTATAAGTTT GACAATCCTG AGACCTTGGC TCAAGACCTT GAAGTCATCA CTGAGGATGT 1680

TCCTATGCTA ATTGAGGTAG ATATTTCTCG TAAGGAACAG GTGTTACCAA TGGTACCGGC 1740
TGGTAAGAGT AATCATGAGA TGTTGGGGGT GCAGTTCCAT GCGTAGAATG TTAACAGCAA 1800
AACTACAAAA TCGTTCAGGA GTCCTCAATC GCTTTACAGG TGTCCTATCT CGTCGTCAGG 1860
TTAATATTGA AAGCATCTCT GTTGGAGCAA CAGAAGATCC GAATGTATCG CGTATCACTA 1920
TTATTATTGA TGTTGCTTCT CATGATGAAG TGGAGCAAAT CATCAAACAG CTCAATCGTC 1980
AGATTGATGT GATTCGCATT CGAGATATTA CAGACAAGCC TCATTTGGAG CGCGAGGTGA 2040
TTTTGGTTAA GATGTCAGCG CCAGCTGAGA AGAGAGCTGA GATTTTAGCG ATTATTCAAC 2100
CTTTCCGTGC AACAGTAGTA GACGTAGCGC CAAGCTCGAT TACCATTCAG ATGACGGGAA 2160
ATGCAGAAAA GAGCGAAGCC CTATTGCGAG TCATTCGCCC ATACGGTATT CGCAATATTG 2220
CTCGAACGGG TGCAACTGGA TTTACCCGCG ATTAAAAATC CAACTTAAAT TTATTAAACC 2280
AGCCTAAAAG GCAATAAATA ATAGAAAAGA GAGAAAAGCT ATGACAGTTC AAATGGAATA 2340
TGAAAAAGAT GTTAAAGTAG CAGCACTTGA CGGTAAAAAA ATCGCCGTTA TCGGTTATGG 2400
TTCACAAGGG CATGCGCATG CTCAAAACTT GCGTGATTCA GGTCGTGACG TTATTATCGG 2460
TGTACGTCCA GGTAAATCTT TTGATAAAGC AAAAGAAGAT GGATTTGATA CTTACACAGT 2520
AGCAGAAGCT ACTAAGTTGG CTGATGTTAT CATGATCTTG GCGCCAGACG AAATTCAACA 2580
AGAATTGTAC GAAGCAGAAA TCGCTCCAAA CTTGGAAGCT GGAAACGCAG TTGGATTTGC 2640
CCATGGTTTC AACATCCACT TTGAATTTAT CAAAGTTCCT GCGGATGTAG ATGTCTTCAT 2700
GTGTGCTCCT AAAGGACCAG GACACTTGGT ACGTCGTACT TACGAAGAAG GATTTGGTGT 2760
TCCAGCTCTT TATGCAGTAT ACCAAGATGC AACAGGAAAT GCTAAAAACA TTGCTATGGA 2820
CTGGTGTAAA GGTGTTGGAG CGGCTCGTGT AGGTCTTCTT GAAACAACTT ACAAAGAAGA 2880
AACTGAAGAA GATTTGTTTG GTGAACAAGC TGTACTTTGT GGTGGTTTGA CTGCCCTTAT 2940
CGAAGCAGGT TTCGAAGTCT TGACAGAAGC AGGTTACGCT CCAGAATTGG CTTACTTTGA 3000
AGTTCTTCAC GAAATGAAAT TGATCGTTGA CTTGATCTAC GAAGGTGGAT TCAAGAAAAT 3060
GCGTCAATCT ATTTCAAACA CTGCTGAATA CGGTGACTAT GTATCAGGTC CACGTGTAAT 3120
CACTGAACAA GTTAAAGAAA ATATGAAGGC TGTCTTGGCA GACATCCAAA ATGGTAAATT 3180
TGCAAATGAC TTTGTAAATG ACTATAAAGC TGGACGTCCA AAATTGACTG CTTACCGTGA 3240
ACAAGCAGCT AACCTTGAAA TTGAAAAAGT TGGTGCAGAA TTGCGTAAAG CAATGCCATT 3300
CGTTGGTAAA AACGACGATG ATGCATTCAA AATCTATAAC TAATTAGAAA TATATAGCGC 3360
TGGAGATGAT TTTATGAAAA AGATTATGAG AAAAATTGCA TCGTTATTAT TGGTTCTAGT 3420

TGTATAATGT AATTACACCG TCGGTAATAG TGCTAGCAGA CCAAAATAAA GCAGATTGGT 3480

CGTATGATGA AAATGCTGTA ATTAACATTT ATGATGATGC TAATTTTGAA GATGGTAGGT 3540

TGCATATGAA CTTTGAACAA TTCTTCAAAT TGGCACAAAT AGCTAGAGAA GAAGGTCTTG 3600

AAATTCATTC TCCGTTTGAG AGAGCTGGTG CGACTAAATC TGCTCGTTAT ATAGCGAAAT 3660

GGATTTTGAG AAATAAAAAA CATTAACAAA TATAGTTGGT AAATCATTAG GACCTAAATC 3720

AGCTGTTAGA TTCGGAGAAG CTTTATCCTA TATTGAAGGT CCTCTTCGCA GAATAAATGA 3780

GACGATAGAT GGCGGTTTAT ATCAAATAGA GCAAATTATT GCATCTGGAT TGAAAGAATC 3840

GGGTTTAAAT GACTGGACTG CGAAAACTTT AGCTTCAGCT ATTCGTGGGA TATTAGATGT 3900

ACTTATTTAG GGGTTGAAAT CATATGAATA TTACCAATTT GTTTTCTATC AAGACAGGAT 3960

GTGATGAAAC TGATAGGCAA CTGCAAAAAC TATTTTTTCA GTTGGATTTA CAATTGGGAG 4020

AATTGACAGA TCAACTAAGA AAATTAGATT CTAATTTTGT TCCTCGTAGT CAATTTGTAG 4080

ACACGTTGGA TTTGAATGAT GTAGAATATA AAGAAATTTT AAACTATTTT ATCTTCCATC 4140

GTAATGATAG TGAAGAAAGT TTGGTAGAAT GGTTATATGA TTGGATTTCC ACAAATCGTT 4200

ATGAACTTCC TAAAGAGTTT TCGATTCGTA TGGCTCATAA ATACCATGAA AGTGTTACTG 4260

AAGTTTTCGG AGATGAATAA CTAAAAAACA GTCATTAGTG ACTGTTTTTT ATAGAAAAAG 4320

AGGTTTTATA TGTTAAGTTC AAAAGATATA ATCAAGGCTC ACAAGGTCTT GAACGGTGTG 4380

GTTGTGAATA CTCCACTGGA TTACGATCAT TATTTATCGG AGAAGTATGG TGCTAAGATT 4440

TATTTGAAAA AAGAAAATGC CCAGCGTGTT CGCTCCTTTA AAATTCGTGG TGCCTATTAT 4500

GCCATTTCCC AGCTCAGCAA GGAAGAACGT GAACGTGGGG TAGTCTGCGC TTCTGCGGGA 4560

AATCATGCGC AGGGAGTAGC CTATACTTGT AATGAAATGA AAATTCCTGC TACTATCTTT 4620

ATGCCCATTA CTACGCCACA ACAAAAGATT GGTCAGGTTC GCTTTTTTGG TGGGGATTTT 4680

GTAACTATTA AACTAGTTGG AGATACCTTT GATGCCTCAG CCAAAGCAGC TCAAGAATTT 4740

ACAGTCTCTG AAAATCGTAC CTTTATTGAT CCTTTTGATG ATGCTCATGT TCAAGCAGGT 4800

CAAGGAACAG TTGCTTATGA GATTTTAGAA GAAGCTCGAA AAGAATCGAT TGATTTTGAT 4860

GCTGTCTTGG TTCCTGTTGG TGGTGGCGGT CTCATTGCCG GGGTTTCTAC CTATATCAAG 4920

GAAACAAGTC CAGAGATTGA GGTTATCGGA GTAGAGGCGA ATGGAGCGCG TTCCATGAAA 4980

GCTGCCTTTG AGGCTGGAGG TCCAGTAAAA CTCAAGGAAA TTGATAAATT TGCTGATGGG 5040

ATTGCTGTGC AAAAGGTAGG TCAGTTGACC TATGAAGCAA CTCGTCAACA TATTAAAACT 5100

TTGGTAGGTG TCGATGAGGG ATTGATTTCT GAAACCTTGA TTGACCTTTA CTCTAAGCAA 5160

GGGATAGTCG CAGAACCTGC TGGAGCGGCT AGTATCGCCT CTTTAGAGGT TTTAGCTGAA 5220

TATATTAAGG GGAAAACCAT TTGTTGTATC ATTTCTGGAG GAAATAATGA TATCAACCGT 5280

ATGCCAGAAA TGGAAGAGCG TGCCTTGATT TATGATGGTA TCAAACATTA CTTTGTGGTC 5340

AATTTCCCAC AACGTCCAGG AGCTTTGCGT GAGTTTGTAA ATGATATCCT GGGGCCAAAT 5400

GATGATATCA CACGTTTTGA GTATATCAAA CGAGCTAGCA AGGGAACAGG CCCAGTATTA 5460

ATTGGGATCG CTTTAGCAGA TAAGCATGAT TATGCAGGTT TGATTCGTAG AATGGAAGGT 5520

TTTGATCCAG CTTATATTAA CTTAAATGGT AATGAAACGC TTTATAATAT GCTTGTCTGA 5580

GGACTAATAA AAAAATATCA TACCTTCATT TTGATTTCCT ATCTATTGAC AAGCATAGTC 5640

ACACTGTCTT TAATACTCTT CGAAAATCTC TTCAAACCAC GTTAGCTCTA TCTGCAACCT 5700

CAAAACAGTG TTTTGAGCAA CTTGCGGCTA GCTTCCTAGT TTGCTCTTTG ATTTTCATTG 5760

AGTATAAGGT ATGATTTGAT TTCTTTTTGT TGACAAATAT ACTATATTAA AAAGATATAT 5820

AAGTAATTAA CTGAGCTTAT CTGTCTTGTC ATCTCTATTA AGGATGGTTT AGATAATCGG 5880

GTGTCTGCTT CTAGGCTAGC ACCTCAATAT CCAAAGGAGT GATGAATTTG AAGGACATAA 5940

GGAATACCTA TCTCTCAGAT GATTTATTGA GGAAGAAAGA TAGGAGTTTT TGAGCTAGTG 6000

AAGGCTTGGA TTTCTAAAGG TTAGAACTAT CATCTTCAGT TCTTAAATCG AAGAAATAAG 6060

CTATCTTACG GAAATAGAGA AGCATTTTTT AAGAACTTGA ATAATTTCGC ACCTTAAGAG 6120

GGTAATAATA CAGTATTTTT ATTAGCAAAT ATTTATGGTG TAGAGGCTAG CAAAACCTAT 6180

ATATTATCGG ATTTAAAAAG GAAGTAAGAA A 6211

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7939 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCGGACTCCC CACGATTCTT CAAAATAACT GAGTATATTT CTATCTTGAT TTTCAGATAT 60

AAATTCTTCC TTCTGTGGCC TCTTCTTACG CTTGAGAAGA GCTTCTCCGA CATGGCTTCT 120

TCCTTACTGA GCAAAACCTT GAGCATAGAT AAGTTTGACT GGCAAGCGTG CTCTTGTATA 180

TTTGGCTCCC TTCCCACTAT TGTGGATAGC GAGGCGTCTT CTCATATCAG TCGTATAGCC 240

TATATAGTAG GATCCATCAC GACACTCCAG AACGTACATA TAAGCCTTAT GATCCATAAT 300

AAATCTCTTC GATTTCGGGC GTATAAGAGC CATCATCATT GTGGACAATC AAAGGAGGTA 360

AGACCTTAAA GCCACTTGTT GAGCCATCCT TGATCGCCTC AATCAAAAGC ATATTGGCTT 420
CCTTTTCTCT TTTTGGATAA ACAAACTGCA GGCGCTTAGG GGCTAGATTA TGTCGTTTTA 480
ACGTATCCAA AATATCCAGA AGTCGATCAG GACGATGAAC CATGGCCAAA CGCCCATTAG 540
ACTTGAGAAT ACTCTGGGCA CTACGACAGA TTTCTTCCAA ATTAGTCGTG ATTTCGTGTC 600
GAGCCAAGAG ATAATGTTCA CTCTCGTTCA GATTAGAATA AGGATTCACC TTGAAATAGG 660
GTGGATTACA CAAAATCATA TCCACCTTAC TCCCCTGAAT GTGAGCAGGC ATATTTTTCA 720
AATCATCGCA GATGACCTGC ATTTGCTCCT CTAATCCATT CAAACGGACA GAGCGTTCAG 780
CCATATCCGC CAAACGCTCC TGAATCTCAA CAGACAATAT CTGTGCTTGA GTACGAGTGC 840
TAGCAAAAAG CCCCACTGCT CCATTCCCAG CACAGAAATC CACAATCAAC CCCTTCTTAG 900
GAAAACGTGG AAATCGTGAT AAGAGAACAC TATCCACCGA ATAGCTAAAA ACCTCTCTAT 960
TTTGAATGAT TTTGATATCT GTCGAAAAGA GCTGGTTAAT GCGCTCTCCT GATTTTAATA 1020
ATTGTTCTTC TTCCATGGTC CTATTATAGC AAATTCATAT TAACATTACA AAAAATATAA 1080
AACTCTAAAC TACTTCTTCT TTTTTAAATG GTGCAGGGCT TCTCCAGTCC AGATTGGTAG 1140
CATTCGTCGA AAGGGAGCAA AGCCGTAGTT AAAGCGGTCG CTTGAAAAGC GTCTCCGTCT 1200
AGGAAACTGG TACTTTTCTT CCTCCAAAGT GCGGATAGAA AGACTGGCTT TCCCTGTAAA 1260
TTCATCTAAA TCCACTACCT GAACTTGAAC CTCTTCATCG ACTTTCAAGG TTTCATGAAT 1320
ATTTTCAATA AATCCTGTCC GAATCTCTGA AATGTGAATC AGCCCCGTAT CACCCGTCTC 1380
TAACTCAACA AAGGCACCGT AGGGCTGAAT CCCTGTAATA CGCCCCTTTA GCTTATCACC 1440
GATTTTCATC TTAGTCCTCG ATTTCAATAG TTTCAATTAC AACATCTTCA ACTGGCTTGT 1500
CCATAGCTCC TGTCTCAACA GCAGCAATGG CATCCAAGAC AGCGTAAGAT GCTTCATCAG 1560
CTAACTGACC AAAAACCGTG TGACGGCGGT CTAGGTGAGG TGTCCCACCT TGATTGGCAT 1620
AGATTTCTGC AATCGGTTCT GGCCAACCAC CACGAGTAAT TTCTTTCTTA GAATAAGGTA 1680
GGTGTTGGTT TTGCACGATA AAGAACTGGC TGCCGTTGGT ATTTGGACCA GCATTTGCCA 1740
TGGAAAGAGC ACCACGGATA TTGTAAAGCT CTTCTGAGAA TTCATCCTCA AAAGATTCGC 1800
CGTAGATTGA CTCGCCACCC ATACCAGTTC CAGTTGGGTC TCCACCTTGG ATCATAAAGT 1860
CCTTGATAAT ACGGTGGAAA ATGACACCAT CATAGTAGCC ATCTTTTGAA AGAGATACAA 1920
AGTTAGCCAC TGTTTTAGGA GCATGTTCAG GGAAAAGCTT GATACGTAAG TCTCCGTGAT 1980
TGGTCTTAAT AGTCGCAAGA GGACCTTCTA CTGTTTCAAT GTCTACTTGT GGAAAATGCA 2040
ATTCTTTTTC TACCATACCA AATACTTCTA AGGCAGCAAA AATGCCATCT TCTTCTAATG 2100
TTTTTGTAAT ATAATCTGCT TTTTCTTTGA TTTTATCATG AGAAATTCCC ATGGCAACGC 2160

TGATTCCAGC ATAATCAAAG AGTTCCAAGT CGTTGAGACC ATCTCCAAAA ACCATGACCT 2220

TCTCTGGTTT CAAGCCAAGG TGTTCCACAA CCTTTTCCAC CCCCGTCGCT TTGGAGCCTG 2280

AAATCGGCAC AATATCAGAC GAATGTTGAT GCCAACGAAC CATGCGAAGT TTGTCTGAGA 2340

GACTGTCAGG CAAGTGCAAG TCATCTCCCT TATCTTCAAA AGTCCACATC TGATAGATAT 2400

CTTCTTTTTC ATGGAAATCG GGATCTACAT CTAAGTCGGG ATAAATTGGA TTGATAGCTT 2460

CACTCATCAT ATCGGTGCGA GTCGACAACT TGGCATCATG ACTCCCAACC AAGCCATACT 2520

CAATTCCTTC TTGCTTAGCC CAAGAGATAT ACTCCTCAAC ATCTGACTTT TCAATCTGAT 2580

GCTGATAAAT GACCTGACCT TTTTTATCTT CGATATAAGC CCCATTCAAA GTTACAAAAA 2640

AGTCAGGCTT GAGATCACGA ATCTCTGGAA CAACACCAAA AATGCCACGT CCAGAGGCGA 2700

TTCCTGTTAA AATTCCTTTT TCACGCAACT GTTTAAAAAC AGTGGGAATT GTAGTTGGAA 2760

TAAACCCTGT CTTTGAATTC CGCAATGTAT CATCAATATC AAAAAAGACA ATCTTGATCT 2820

TCTTTGCCTT GTATCTTAAT TTCGCGTCCA TCTCACTACC TCTTTCAATC TAACTCTTTC 2880

CATTATATCA TAAAGTAGGC AAATCCCCTA TTTTCAAAAA GTTTATCATT TTTATTTTAA 2940

TTTCTTGGAT GAGAAAAGAG ACATATTTAT GAAAAAGCTC CATCGTGCTT TTAATGTGTT 3000

CTCTTGTTTT CAAACTCGTA AAAAGGGAGC CACTGATCCT AACTCGCTCT CTCATTTCAA 3060

AGCTTGTGAA AAAAGACCCG TTGGGGTCTT AATTCGCTTT CTTGTTTTCA AGCTCATGAA 3120

AAAGAGACCC AACTGGGTCT TTTCTTTAAT CTTCGTTTAC GAAAGGCATC AAAGCCATTA 3180

CGCGAGCGCG TTTGATAGCT GTTGTTACTT TACGTTGGTT TTTAGCTGAA GTTCCTGTTA 3240

CACGACGAGG AAGGATTTTC CCACGTTCTG AAACGAAACG GCTAAGAAGC TCAGTATCTT 3300

TGTAATCAAC ATATTCAATT TTGTTTGCTG CGATGTAATC AACTTTTTTA CGGCGTTTGA 3360

ATCCGCCACG ACGTTGTTGA GCCATGTTTT TTCTCCTTTA TAAGTTTAGT TGTCCATTAG 3420

AATGGTAAAT CATCATCTGA AATATCCAAT GGGTTTGTTG CTCCAAATGG ATTTTCATTA 3480

CGTGAAAAGT CTGGTACTGA ATTTGTAGGT GCTGAATAGT TTGCAGTTGG TGCAGAGTAA 3540

GCTCCACCTG TGTGACCCTC ACGCACACTA CGGCTTTCCA ACATTTGGAA ATTCTCAGCC 3600

ACGACCTCTG TCACGTAGAC ACGTTGTCCT TGCTGGTTAT CGTAACTACG AGTCTGGATA 3660

CGACCTGTCA CCCCGATAAG TGAGCCTTTT TTAGCCCAGT TAGCAAGATT TTCAGCCTGT 3720

TGGCGCCACA TAACGACATT GATAAAATCA GCCTCACGTT CACCATTTTG ACTCTTAAAT 3780

GTACGGTTTA CTGCAAGAGT AAAAGTCGCA ACTGCTACAT TTGATGGGGT ATAACGCAAC 3840

TCAGCGTCAC GTGTCATACG CCCTACAAGT ACAACATTGT TAATCATAGT TTACCTTCTT 3900

ACGCGTCAAT TTTGACGATC ATGTGACGAA GAATGTCAGC GTTGATTTTT GAAAGACGGT 3960

CAAACTCTTT AAGAGCTGCA TCGTCATTTG CTTCAACGTT AACGATGTGG TAAAGTCCTT 4020

CACGGAAATC TTGGATTTCG TATGCAAGAC GACGTTTTTC CCAAGTTTTT GATTCAACAA 4080

CAGTTGCACC GTTGTCAGTC AAAATAGAGT CAAAACGTGC TACCAAAGCG TTTTTAGCTT 4140

CTTCTTCAAT GTTTGGACGA ATGATATAAA GAATTTCGTA TTTAGCCATT GATATGTTCC 4200

TCCTTTTGGT CTAATGACCC CAAGACTTTG CAAGGGGTAA GTGAGGTTCG CTCACAATAA 4260

ACTATTATAC TAGAAAAAAT TTTTTTACGC AAGTAAAAAC ACTAGAATTC GAAAAAACGC 4320

CACATGGGCG TTTTCCTGTT CTTATGGTTT GATACGGTGC AACATACGTG GGAATGGAAT 4380

AGCTTCACGG ATATGTTTTG TTCCTGCTGC GAAGGTTACC ATACGTTCGA TACCGATACC 4440

AAATCCTCCG TGTGGAACTG TACCGTATTT ACGAAGGTCA AGGTAGAATT CATATTCTGT 4500

ACGATCCATG CCAAGTTCAT CCATCTTAGC GACAAGGGCA TCGTAATCTT CCTCACGCAT 4560

AGACCCACCG ATAATTTCTC CATAGCCTTC TGGAGCAAGC AAGTCTGCAC AAAGCACGCG 4620

CTCTGGATTT CCAGGAACTG GTTTCATGTA GAAGGCCTTG ATGGCTGCTG GATAGTTCAT 4680

GACAAATGTT GGCACACCAA AGTGGTTTGA AATCCAAGTT TCGTGTGGTG ACCCAAAGTC 4740

ATCACCATGC TCAAGATGCT CGTAGTCAGC ATCTTCATCA TTTTCATGCT CTTGCAAGAG 4800

GTCAATGGCT TGATCGTAAG TGATACGTTT GAATGGCTCT GCAATGTAGC GTTTCAAGAG 4860

TTCTGTATCA CGTTCCAAGG TTTCCAAGGC TTGAGGCGCG CGGTCAAGAA CACCTTGTAG 4920

AAGAGCTTTC ACATAAGCTT CTTGCAAGTC AAGCGACTCA TCATGTGTCA AGTATGAGTA 4980

CTCAGCATCC ATCATCCAGA ACTCAGTCAA GTGACGGCGT GTTTTTGATT TTTCAGCACG 5040

GAAAACTGGA CCAAAGTCAA AGACACGACC AAGAGCCATA GCCCCTGCTT CTAGGTAAAG 5100

CTGACCTGAT TGGCTCAAGT AGGCTGGCGT TCCGAAGTAG TCAGTTTCAA AGAGTTCTGT 5160

AGAATCTTCT GCCGCATTTC CTGAAAGAAT TGGGCTGTCA AACTTCATAA AACCGTTCTT 5220

GTCAAAGAAC TCATAAGTTG CATAGATAAT AGCGTTACGG ATTTGCAACA CAGCTACTTG 5280

CTTACGAGAG CGTAgCCACA AGTGACGGTT ATCCATCAAA AAGTCTGTTC CGTGTTCTTT 5340

TGGTGTGATT GGGTAGTCTT GAGATTCACC GATCACTTCG ATGTCTGTGA TGTCCAACTC 5400

ATAGCCAAAT TTAGAACGTT CGTCCTCTTT GACAATACCT GTCACATAAA CAGACGTTTC 5460

TTGGCTCAAG CGTTTGATAA CATCAAACTT CTCAAGTCCC ACTTCTTCAC CAAATTTTTC 5520

GACAAAGTTT GGTTTAAAAG CCACACCTTG AAAGAAGGCT GTTCCATCAC GCAATTGTAA 5580

GAAAGCGATT TTTCCTTTTC CTGATTTGTT GGCAACCCAA GCGCCAATCG TCACTTCCTG 5640

ACCAACATAG TCTTTTACGT CAATAATCGT TACACGTTTT GTCATTATTT TTCCTTTTCT 5700

TTTTTATTCT TTATGGCAAA CCACCTCTAT ATTGTTCCCA TCCAGGTCAA TCATAAAAGC 5760

AGCATAGTAA ATCGGATGCT CACTTCGATA ACCAGGAGCC CCATTGTCTC GCCCACCTGC 5820

CTCTAAGCCA GCCTCATAAC AAGCCTGAAC TTCTTCCTTA TTTTCTGCTA AAAAAGCAAA 5880

ATGAACAGGA TCTTGTGTTC CCTGAGTCAG CCAAAAATCA CCACCAGGAT GAGGGCTGTT 5940

CGGGGATAGA AAACTAATTA GAGAACTAGT CTTAAAAGCC AATTTATAGT CCAAAGGAGC 6000

GAGAAAACTC CTATAAAATC CTTATGAAAT TTGTAAATCC TTTACCTTAA TCTCAAAATG 6060

ATCAATCATT CTCACTACCC ATAAATGCTT TCAAGCGTTC GACTGCTTCT TTAAGCGTGT 6120

CTAGGTCTGT CGCATAGCTG AGGCGGACAT TTTCTGGTGC TCCAAATCCA GCTCCTGTTA 6180

CCAAGGCCAC TTCGGCTTCT TCTAAGATAA CAGTTGTAAA GTCTGTCACA TCCGTGTAGC 6240

CTTTCATCTC CATGGCCTTT TTGACATTTG GGAAGAGATA GAAGGCCCCT TGCGGTTTGA 6300

CCACTTCAAA TCCTGGTACC TCTGCAAGGA GGGGATAGAT GGTATTAAGA CGTTCCTCAA 6360

AGGCCTGACG CATGCTTTCT ACAGTATCTT GCTCACCTGA TAGAGCCTCA ACTGCTGCAT 6420

ATTGGGCTAC TGCTGACGGA TTCGAAGTTG TTTGACCTGC AATCTTGGAC ATGGCAGCGA 6480

TAATGTCTGC TTCTCCAACG GCATAACCAA TCCGCCAACC AGTCATGGCA TAAGTTTTAG 6540

ACACACCATT GATGACCACT GTTTGCTTGC GAATCGCTTC CGATAGGCTA GAAATCGGTG 6600

TGAACTCATG ACCATTATAA ACCAAGCGGC CATAGATATC GTCTGCTAGG ATGAGAATAT 6660

CATTTTCTAC AGCCCAGTTT CCAATTGCCA AGAGTTCCTC ACGGGTGTAA ATCATACCTG 6720

TGGGATTAGA TGGCGAATTC AGCACCAAAA CCTTGGTCTT GTCAGTGCGA GCTGCTTCTA 6780

ACTGCTCTAC GGTCACCTTA AAGTGATTGT CTTCCTTAGC AGAAACAAAG ACGGGAACGC 6840

CTTCTGCCAT CTTGACCTGA TCTCCATAGC TAACCCAGTA TGGGGTTGGG ATGATGACTT 6900

CATCACCTGG ATTGACCACA GCCATAAAGA AGGTATAGAG AGAATATTTG GCTCCCGCAG 6960

CGACTGTCAC TTGATTTGAC GCTACAGAAT AGCCGTAAAA GCGCTCAAAG TAGCTATTGA 7020

CCGCCGCCTT AAGCTCTGGC AGACCTGAGG TTACTGTATA AAAAGAAGCA CGCCCATCTC 7080

GAATCGATGC AATGGCGGCA TCTTGGATAT TTTTGGGAGT AGTGAAATCT GGCTCACCCA 7140

AGGTTAGAGA CAAAATATCT CTACCCTCAG CCTTCAGTGC TTTGGCACGG GCTCCAGCAG 7200

CCAAAGTCAC ACTTTCTTCC ATTTCTAAAA CACGGTTGGA TAGTTTCATA GGCCCTCCTT 7260

GTTGACCAAT GCTCCTGTTT CAAAATCTAC TAGATAAAAA TCAGATCCTG ACTTAACTTC 7320

CCAGATTGGC TTATCTTGAT AACGGCCAAA GGTTATCTTG TCAATCTCGC CAGCTCCCTT 7380

TTCCTTAGAA ACCGTTTCTG CTTTTTCTTG TGAAACACCC TGATTTAGCT GATAAACGTA 7440

```
AATCTTATGG TCATCTTTAC CAATCAGGAC AGCAAGCGCT TCTTGCTGTT TGTTACGACC    7500

AAGAACGCTG TAATAAGATT CCAAGCCATT GTATAAATCA ACCTGATCAG CCTGCTCTAA    7560

TCCTGCATAC TGCTGAGCTA ATTTTTCTCC TTCACTTTTA GCTGTTTGAT AGGGTTTCAT    7620

GCTAAGAGAA ACCATATACA GAAAGGAACC ACTGATAACC ACAAACAAAA TCGTCATCCC    7680

TAGACCATAC TGCCACAGTA GATTATTTTT TGCTTTGTTT TGTCTTTTTT TCACTCGTCT    7740

ATTTTACCAT CTATTAAGCT TTATTACAAG TGAATATAAG AATACTCTTC GAAAATCTCT    7800

TCAAACCACG TCAGCTTTAT CTGCAGACCT CAAAGCTGTG CTTTGAGCAA CCAATTCTAT    7860

TTCTCCCTTC AAACAAAACC GATTTTGAAA GTGAAACAGT TCTTACTTTT TCAGTCACAA    7920

ATGATTAGAG TTTGCCGGG                                                 7939
```

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```
CCGCTCTACC GTCAAATAAT TACCATTTTG TTTAATACCG AAATTTTTAT CTACTGAAAA      60

TTCAGTTGGT CTGTTGGTAC GATCGTCGTA TACAGTACCA TTCTCACGAA TAGTATAATT     120

GTAATCAGTA TCACCTTGTT TCCTTAATTT AAGGTAATAA TTACCATCAA TTTGTTTATA     180

ACCTGAATCT TTTCTAGTTG CTTCTCTAAA ACTTACTCCA GCAGGCATCA CATCAGCAAA     240

CATGAGTACT TGTTTGTTCT TTTTTTCAAC AATAACAGAG TCAATATAGG TTGCACCACC     300

GCTGATTTGT AAGTCACGTC CACCAACTTC ACGAGGCCAT TCTAATGGTA CTGGCGCAAA     360

ATCATCGAAT GCCAATGTTA ATTTTGGTTT AGTCCATGTC TTACCATTAT CATCACTATA     420

ACTTGTAGCA ATATTAATTT TATTCAAGAA ATCATGAGTT CCACCGTAAC GAGCGTCAAT     480

GCTTGAAAAT ACCCGACCAT TGCTAAAAGT ATACAGAACT GGAATACGGA AATAGTTAGA     540

ACCTGTTGTA TCATTAGCCG TATAAATTAA ATGTCCAGTA ACAGCGTTTG TTGTCATCTT     600

TTTAACAGTT TCTTCATCCA ATGCACTATT AAAGAATTTG ATATTTTCTA GTGTTCCGTT     660

AAAACCAAAC GCCGTTTTTC CTGCACGTTT CACTCCCCCA AGCATATAGT AATCAATACC     720

TTTAATATCC TTGATGTTTA GGAAATTATC CACTTTCTTT TCTACTACTT TTGTACCATT     780

TGCGTATAAA GAATATGTTT TTTTGACTGA ATCTGCTACT ACTGCAACAG TGTTAGTCAC     840

AGCCTCTTGT TTGTACTTAC CCCAAACTGA AGCAGGTCTG GATACTAGGT TATTTTTATT     900
```

GGAAGAAGTA TCACGCGCTT CCATCCCCAA CTCACCATTG TCTCTAAGGA ACACATCTAC 960
ATAACTATTT TGTTGACCGG GTTTGGAATT AGATATTCCA AACAGAGCTT GTAAGCCTTT 1020
CTCACTTGAC TGATTGTACT TAATCACTAC AGTAAAGTCA CCGCTAGTAA ATTTATCCTT 1080
TAACTCTTTA GTAACATTTT CTCCGCCCCC TGTTAAAGTA ACATTATTTT TTTCTAAGAC 1140
AGGAGTTTCT TCCGCTGTAG AAGATGGATC CTTAACAGTA GTTTCAACTG TTCGAGGTTG 1200
TACAGTAACT TCCGAAGAGT TATCCGATGT AGGTTGTACT TCCGAAATCG GAGTCGTTGG 1260
TGCAACAGGT TGCACCAACT TTGGTGTTGA TACTTCAGAA GTTTCAGTCT CCTGAGCTGC 1320
AACTGAGTTA GCAACAAATG CTGATAATAC CACTACAGTA CCTAAGGTTA CATATTGTTT 1380
AATATTTTTT TTCATTTTAT TTTTCCTCGT TTAAAACTTT GATAACAAGT TTTTTAACAG 1440
TTTCATCATT GCAATGAATC TTTGGTTGGT GAAGATCTTC TTCAAAAGTC ACCAACATAT 1500
TCCCTGGAAG CAATTCAACA ATTTGATAGT CTTTGCTATC GTAAAAAGCA ATATCCTTCT 1560
CTTCGCTAAA AGGTACACGT GACTGGGCAC GAACTGGGGA AGTTACTGCC ATTTTTTCAG 1620
TATTTTCAAC AACAATATGA ATATCTAAAT ATTTCTTATG AGTTTCAAAA ATATCTCCTG 1680
GAACTCCATC AGCTAGATAA GTCATACAAT TTGCAAAAAC ATTTTCCCCG TCAATATCAA 1740
TTTTTCCATC AACTAAATCT GTCAAATTTG TATTTTCTAA AAAATCACAG ACTTTTGAAA 1800
AATATTTATT GACAGAAGCA TATCGTTTAA AATCAGATTG TTCAGAAATA ATCATATTAT 1860
TTTCTCTTTT CTATTAGTGA CGAACTTCCC AACTTGAATC CGCTTTAATT TCTGTAATAT 1920
CATGAATCGT TGTATATTTA GGTGCAGATA CTTTATTTCC AGTAAGAACA GATACAATAT 1980
AACCTGAAAC TACTGATACA GAGATTGAAA TCAATGAATA TGCCCAGTAG CTAACAGCTG 2040
TTGGAGGAAG GAAGTATTTA ATAAATACCA TGACGATGGT TGATACAATC AGCGCTGCAT 2100
AAGCACCTTG TTTATTTGCT TTTTTAGAAA CAAATCCAAG AATAAATACA CCACCAAGTA 2160
GACCAAGTAC AAGTCCCATG AAACTATTGA ACCATTCGTA TGCAGATTTA ATATCTGAGT 2220
GAGCCATGAC AATGGAAACA CCAATTGAGA ATAAACCTAC TGCTAGAGAT ACGAATTGTG 2280
CAATTTTCGT ACGACGATTG TCTGACATAT TTTTAGAAAT GACATCTTGA ATATCCAATG 2340
TCCATGAAGT TGCAACAGAG TTCAAACCTG TTGAAATAGT TGATTGAGAT GCTGCATAAA 2400
TCGCTGCCAA GATCAAACCT GTGATACCTA CTGGTAACTG GTATGCAATA AAGTACATAA 2460
AGATTTGGTC TTGAGGGATA TTGCTAGCTG CACTATCTGC ATTTTGTACT TGATAGAATA 2520
CGTACAAGCC TGTACCAATC AAGTAAAAGA CTGTTGCAGT TGCAAGTGAC AAAACACCGT 2580
TTGTGAACAA CATCTTATTA AGTTTCTTAA TATTTTGTGT TGTAGTAAAA CGTTGAACCA 2640

```
AATCTTGAGA TGAAGCATAG GAAGACAAGA TTGTAAAGCC TGAACCCATC ACAATTAAAA   2700
AGATGGAGTT TGAAAGCAAG TTAGGATCGA AAAGTTTTTC ATTTGCAGCA AGGAATTTCC   2760
CGTTTGCTAA TGTTTCTGCT ACTGCACCAA AGCCACCTTT AATATTAGCA ATCAGTACAA   2820
ATAAAGCTAA AACGACACCA CTAATCAGAA TCACACCTTG AATAAAGTCT GTCCATAATA   2880
CGGATTTTAG ACCACCAGTA TAAGAATAAA CAATTGCAAC TACACCCATC AAAATAATCA   2940
AAATATTGAT GTCAATTCCT GTCAATACTG ATAAACCAGC TGATGGGAGG TACATAATGA   3000
TAGACATACG TCCCAATTGA TAAATAATAA ACAAGAGTGC TGAAATAATA CGAAGTGCTT   3060
TAGAATTAAA ACGTTTATCC AAGTAATCAT ATGCCGTATC GATGTCTATC CGTGCAAAGA   3120
TAGGTAAGAT AAAACGAATT GTCAGTGGAA TAGCTACTAC CATCCCTAAT TGAGCAAACC   3180
ATAAAATCCA GCTACCTGCA TAAGAGCTAC CAGCGAGTCC CAAGAAGGAA ATCGGACTGA   3240
GCATTGTGGC AAAAATGGAT ACCGAAGTAA CATACCAAGG AACCGAACCA TCTCCTTTAA   3300
AGAACTCTTT TCCTTTCATC TCTTTTTTAG AGAAATAGAT ACCTGCAACC AACACCGCAA   3360
GTAAATAAAC AATCAAGATA ATTAAGTCAA TTATTGTAAA TCCTGTTGTG CCCATAACAT   3420
ATCTCCATAT TGATTTTATT TATTATAAAA ATTCTTTTCG TGCTTGTTGA ATAAGTTCTG   3480
CTGCTTGTTT TGCAACTTCC AAGTCACCTT CTGCCAATGC TTCTAAAGGT TGACGAACAG   3540
AACCTAAATC AAGTTTTTCA TTTAGACGCA AAACTTCTTT TGCTACAGCA TACATATTTG   3600
CCTTACCTGA TATCATCTTA TAGATAACTT CATTGATAGC ATATTGAAGT TTTTTAGCTG   3660
TATCTAAATC TCGTTCTTGA ATCAAACTTT CCAATTTCAA GAACAAATCT GGCATAACGC   3720
CATAAGTACC ACCAATACCA GCTTCTGCTC CCATCAAGCG ACCACCAAGA TATTGTTCAT   3780
CTGGACCATT GAATACAATG TAATCTTCTC CACCTGCAGC TACAAACATT TGAATATCTT   3840
GTACAGGCAT AGAAGAATTT TTAACTCCAA TCACACGAGG ATTTTGACGC ATTGTTGCAT   3900
ACAAACTACC AGTCAACGCA ACCCCTGCCA ATTGTGGAAT ATTATAGATA ATAAAATCTG   3960
TATTTGACGC AGCTTCACTC ATTGCATTCC AATATGCTGC GATTGAATAC TCTGGCAATT   4020
TGAAATAAAT AGGTGGGATA GCTGCAATAG CATCGACTCC AACACTTTCT GAATGTTTTG   4080
CCAATTCGAT ACTATCTTTC GTGTTATTAC ATGCAATATG GTTGATAACT GTTAATTTAC   4140
CTTTAGCAAC TTCCATAACA GCTTCAATAA TTTGTTTACG ATCTTCTACA CTTTGGTAAA   4200
TACATTCACC TGAAGAACCA TTTACATAGA TACCTTTTAC ACCTTTGTCA ATGAAATATT   4260
GTACCAGAGA TTTTACACGA TCTTGGCTAA TTTCACCATT TTCATCATAG CAAGCATAAA   4320
ATGCAGGGAT AACGCCTTTG TATTTAGTTA AATCTTTCAT CAGATTTCTC CTTTATATTG   4380
TTTTTTATTT GATGACATTA ATAAATCGCT GAGCAATTTC TTTTGGACGT GTAATCGCTC   4440
```

CACCAATGAC TACACTGGTA ACACCTAAAC TATAAGCTTT TTTTAATTGT TCTGGATAAT 4500
GAATTTTTCt TCGGCAATTA CCGGAATATT AAAATCAGCC AATTTTTTCA TTAGTTCAAA 4560
ATCAGGCTCA TCTGATTGTA CACTTGTACT TGTGTAACCT GATAATGTTG TACCAACAAA 4620
ATCAACGCCT GATTTAAATG CATAGAGACC TTCATCTAAA TTACTTACAT CCGCCATCAG 4680
CAATTGATTC GGATATTTTT CTTTTATTTT TTTGATAAAT TCACTGACAA CTAAGCCATC 4740
ATATCTTGGT CTTAAAGTTG CATCAAATGC AATGACTGTT GTTCCGCATT CTACAAGTTC 4800
ATCTACTTCT TTCATCGTAG CAGTAATATA TGGTTCTTGA GGTGGATAAT CCCTTTTGAT 4860
AATTCCAATT ATTGGTAAAT CTACTACTTT CTGAATTGCT TTAATATCAC GCACAGAATT 4920
TGCGCGAATG CCCACTGCTC CTGCCTCTAA AGCTGCTTTA GCCATAAAAG GCATCAAGCT 4980
AAATTCTTCA TTATAAAGGG CTTCACCAGG TAAAGCTTGA CAAGAAACAA TGACTCCACC 5040
TTGAACTTGG CTTATAAATT TTTCTTTAGT CCAAATTTGG CTCATTTTAT TATTCCTCCT 5100
TATGGATAAT AGTTTGATTG TAATAATATT GTCTCTCTGG ACTTTCCAGA TAATTAGAGA 5160
ATAAGCAGTC TGTAATTAAA AGTATTGGAA ACTGAGGTGA TATGCGATTG CCATACGAGA 5220
GATGATCGGT CGAAGCTAAT AACAATAGTT CATCAAAGAA ACAATCTTCT TCGTCAAATT 5280
TTCTTGTAGT CATTAAAACT GTTTTAGCGC CTTTATCTGC AGCTTTTTGT AGACCTTCTA 5340
GTACAATATC AGTTTGACCT GAAATGGATG CTCCAATGAC AAGGCAATTT TCATTAAGTA 5400
GTAAGCTACT CCACAAAATC ATATCCTCGT CTGATAATAC TTCACCAATC ACTCCGAGAC 5460
GCATAAATCT CATCTTCATT TCTTGTAAAG CAAGAACAGA ACTTCCTTTA CCGTAGAGAT 5520
ATACACGCTC AGCAGTTTCT ATCATCTCAG CAATACGCTC AAGTTGAACT TCATCAAGAA 5580
CCGTGTAAGT TTTTCTCAAC ATTTCCTCAT AGTCGGATAA AACTTTTTCT GTTGCCTCTG 5640
TATATAATGC CAACTTTTCT TTCTCATGAA TCATCTCTTG GTATTTGAAA ATGAATTGTC 5700
TAAAACCTTT AAAACCACAT TTTTTCGCAA ATCGAGTCAA TGTTGCTTTG GATACATTAA 5760
GGTATTCGCA CAATGCTTTA GATGAATAAT CATTCAGAGG TTGCTGTTTT AAGAAGAATT 5820
TAGCAATGTC TTTTTCAGCA TATGCCATAT TTGGTAAGTT AGCTTCTATC ATTGGAATTA 5880
GTTCTTTTTG CAGTAACATA TGAGCTCCTT AGTTGAAGTA AACGTTTACA TTCTTTATTT 5940
TAACACTTTT TTTTTTTTTC AATATTTTTC ATAAATTAGA AACTAGTTTC CAATTTCTTT 6000
CGTTTCATAA CAGAACAACA AACATAAAAA TATAATAGTT TTTATTCTTT TTATCGTAAT 6060
TATATGTATT GTAAGAACGT TTATCACTAA TAATATGTTC ATATTAAAAT ATTTTAGTAA 6120
TATTTTATTT TGGTTTTATT ATTTCTTTTC GGAATTTCTA TATAATATTT TATTTCTAAA 6180

AAAATTGAAA AAATATTTCT AGTTTCTTTA TTTTATATAG GTAATATATT TTATTTCTAA 6240

ATTAAAAGAG AATCCCATAA AAACTACAGA TTTATGAGAT AAATCAGGTC ACCTATTTTA 6300

AAAAAGCAGC AAACTATAAA CTAAAAAGTT CCACACCAAA TGTAACCCCA TACTTCCCCA 6360

TAAGTCAGAT TTATAGCGCA CCATACCTAA AAACATTCCA AGTGAAACGT ACAGACACCA 6420

AGCTAGAATG GTTCCTGGAT GATGTACTAA GGCAAATAAA ACACTTGTCA AAGCAACTCG 6480

AATATCTAAT TTTCTAACCA AGTTCCATAA AATTTCACGA TACAGAAATT CTTCAACCAT 6540

ACTCGCATTG ATTAAGAACA ATAAAAATGA AAACCAAGGA ACTTGATGTT GAAGGCCAAT 6600

TAAATTTGTT TGATTCGTGC TTCCTTGAGC ATGAATCAGG CTAAAACATA GACTTATAAT 6660

CAGTAGACTA GCTAGTCCAA TACCAAGGCA TTTCATCCTA GTTTTCATAT TGACCTTGAC 6720

CACTTGTTTT CGTTGACCAT ACATCCATAA AAAAGAAAAA AGAGACGCAC CATAGAGAAC 6780

CTGTAGTATA GTTAACTCAC CGATACAAAG AAATTTCAAT AAGTATAGAG ATACCAATAG 6840

GACATTTACT TGTTGGAATA TATAAACTGG AATTATTCTT TTCATAGTTA CCTCCGAAAT 6900

AAATCTTCAT AATCTAAATC TAATATCTGC ACAATCCTTT CTACCCATGG ACTTTGAGGC 6960

ATTCGTTGTT CCATCTTGTA GTGGCGAATC TTTTGATATA AACGATTCAA TTCACTTGGA 7020

TAGTGAAACT CTCCCGCAAA CATTTTTCTG GTTAACTCAA TCCAGCTGAT ATTTCTTTCA 7080

GCCAAAATAA TGGACAAGTT CTCCCAAAAT CGTTCAGCCA TATTrCTTCT CCTTTAGTTA 7140

GATAAATAAT GTGTTTGyGC CATGTAAATC AATTGTTTCG TATCTCTTGG CAATAGAGCT 7200

CTAGCCTCTT CCAAATTCAG ACTTGGATAA ACCCGCTTAT TTGAAACCAC AAAAGGAAGT 7260

CCGATGGTTA GTTCAGGATT TTTTAAAATT ATCTCAACGA AATCCGTTAA TCTTAGATTG 7320

TCACGGTTCT TAAATCGTAA TAAATTGGGA GATAAAAACT CAAAACAATC TGAAGAATAG 7380

CTCATCATCT CAATTAATTT GTCCTTTGTC ATTTCAGAAA CTGAATGACA AGATACCTCA 7440

ATGCCATAGT TTTGGAAGAA GTCTAAAAGA AGTTGATTTC TTTGGCTATT TTTACTTAGA 7500

TAGAGATCAA TCATGGGAGA CCTCCAACAA ATTTGCTTCC ATTTGATATT CTGAGACGAT 7560

TAAGGAATCT AACAACTTTG AGAAGTTAAT CGATTTCTTG TCTTCATCAT AAGCTTTTAC 7620

AGTTACTTGG GTTGTAAGTA TCCCCTCTTT TCCCTCGGCT CGATAGTCTT GTCAATATAA 7680

AACAAAAACA AGATTCTGAT TATCATCTAC AAAGGCATTA ACTCCGTTCT TTATATCCTG 7740

ACTTTCAAGG AATTCCATAA CGTTTTGAAG ATAGGATTCA TAAAATAGTG GGTAATTATG 7800

TTTTTTATGG TAATCATCTA AAAATGTTAC CTCAAACTCA CATGGATAAT TGGGCATCAA 7860

AAATATTTGT TCATCCAGCT GTTTGATTTC TGCATCATGT AATTCTGTTT CTAATTCATC 7920

ACAATCTAGT ATTGATTCTT TATTTAATGC TTTTATCTTT TTCCTCTATT TCTTTTAATT 7980

TCTTTGCGAT TGCGGCAATC ACAGGAACGG TTACACTATT ACCAACTTGT TTATAGAGCT 8040
GACTATTAAT AGAGACTTTT CTAGCAGCTT CAAAAGCCTA ATCAGGAAAG CCATGCAATC 8100
GAAAACACTC TTTAGGAGTG ATTCGTCGTA TTCTCAAACG GTAAAATTGT CCATCTATTA 8160
AAACACCAGC TACTTGGTAA ACTTGTTTAT CTTCTCCTTC ATAGCTAGCC ACTACTACTC 8220
CCATTTGACC ACTAGTTGTT AACGTATTAG CTATACCTTT TCCAACTCTA CCACGACGAT 8280
ACTGAGAACT TGGTCTTTCT AAATTGATTG AATCCCCAAT CTCTGCTTGA GCATATCCTT 8340
TTTTCGTTGC TTCCCGTACT TTTAGAAATT GGATTGGTTC TGGAATTAGT ATTTTGGGGA 8400
TTTTATCTCC TCCTTGCATC GTAGTCAGTG TTGGAGATAA GCCCTCACTT CCATAGACAC 8460
GACCTGTCTC CTTAAAGCTA GTCGGTAAAT CTCCAACAAC GACAATGCCA TAACGATCCT 8520
GAGTATTTAA AGTAAACATC GGCTCTTGAT TTTCCTTAAA GCGTCTCCCA TTTTGTCTCT 8580
TGTCTAATCT ATCTGGTGTC ATACAAGGAA TCGCAACTTT AAATCCTTCT CCTTTACCAC 8640
GAACTAAGGT TGGCGCAAGA CCTTCTGAAT AATAGACTTT ACCGCTCATT CCACTTCTTG 8700
ATGGATTCAA ATTTCCTAGT GCTTTCAAAG TCTCAGAGTT AGTTGCTTGA CCTTCTCGTC 8760
TGAAAGGAAA TAAGAGTCTG GTACCTTTCT TTCTAGAATG TCCGATAATA AACACCCTCT 8820
CTCTGTTTTT GGGAACGCCA AAATCCTTAC TGTTAAGCAC CTGCCACTCA ACATCAAACC 8880
CCAACTCATC AAGTGTGGTA AGTATTGTGG TGAACGTCCG TCCCTTATCG TGATTGAGTA 8940
GGCCTTTAAC ATTTTCAAGA AAAAGAAAAC GTGGTTGGAT TTGTTTGGCC GCCCGAGCAA 9000
TTTCAAAGAA CAAAGTTCCT CTAGTATCTT CAAATCCCAA TCGTCTTCCT GCGATTGAAA 9060
ATGCTTGACA AGGGAATCCC CCACAGATGA CATCGACTTT CCCTCTAAGT TTTTTAAATT 9120
CGTCATCTGA AACATCTCGT ATGTCATGAA ATTCTATTTC TCCTTCCGTT TGAAAAATGG 9180
ACTTATAAGA TTTCCTAGCA AATTTATCAA TCTCACAAAA TCCCAAGCAC TCATGCCCTT 9240
GAGCTTCCAT TCCCATCCTA AAGCCTCCTA TCCCAGCAAA TAAATCTAAA ACCCAAATCA 9300
TTCATACCTC TCTCAACTAG ATGTAACTTA CAAAACCCCT GACCTCATGA GCCACTTTCT 9360
TCCTCCTCAT GAGGTCAGTT TTACTTTCTG CTGTTCCAGT ATCGTTTTTC CTCGCTAGAT 9420
TTCCTCAAAA GGGCAGACTC CTCCCTTGGT TCGTCACACG ATTTTTTCAT CTCGACTGTT 9480
CTTTAATGCA TCATTAACGA CGCTTTTCTT CTAGGTGGTT CATAAGGAAC AGGAAGATTC 9540
AGGTTGACTT TTCTAATCCT AGAATAAAGT GCTGAAAACA ATTCGGAATA GGCATAGAGA 9600
CTAGACAATT TGAGGAGCTG CTTGCGTCCT GTTCGAACAC ATTTTCCTAC CACGTGAAGA 9660
AAAAGATGGC GGAAGCGTTT GATTGTTAAA GTTTGGAAGT CACCTCCAGC TAGATGTTTG 9720

AGAAAAAGAT AGAGATTGTA GGCGATACAG CTCATCATCA TACGAACTCG TTTTTGATTA 9780

AGGTTGAACT ATCCGTTTTA TCGCCAAAAA ATCCCTCCTT CATCTCCTTG ATGAAATTCT 9840

CGGCTTGACC ACGTCCACGA TAAAGCTGAA ACTGGTCTTG GCTTGTTCCG GTACCGA 9897

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CCGTGGAACA AGCCAAGACC AGTTTCAGCT TTATCGTGGA CGTGGTCAAG CCGAGAATTT 60

CATCAAGGAG ATGAAGGAGG GATTTTTTGG CGATAAAACG GATAGTTCAA CCTTAATCAA 120

AAACGAAGTT CGTATGATGA TGAGCTGTAT CGCCTACAAT CTCTATCTTT TTCTCAAACA 180

TCTAGCTGGA GGTGACTTCC AAACTTTAAC AATCAAACGC TTCCGCCATC TTTTTCTTCA 240

CGTGGTAGGA AAATGTGTTC GAACAGGACG CAAGCAGCTC CTCAAATTGT CTAGTCTCTA 300

TGCCTATTCC GAATTGTTTT CAGCACTTTA TTCTAGGATT AGAAAAGTCA ACCTGAATCT 360

TCCTGTTCCT TATGAACCAC CTAGAAGAAA AGCGTCGTTA ATGATGCATT AAAGAACAGT 420

CGAGATGAAA AAATCGTGTG ACGAACCAAG GGAGGAGTCT GCCCTTTTGA GGAAATCTAG 480

CGAGGAAAAA CGATACTGGA ACAGCAGAAA GTAAAACTGA CCTCATGAGG AGGAAGAAAG 540

TGGCTCATGA GGTCAGGGGT TTTGTAAGTT ACATCTAGTT GAGAGAGGTA TGAATGATTT 600

GGGTAAATAC AATGAGCTTG AAAGAAGTAG CAAACTCACC AAGCGCCAAT TCTTTGAGAA 660

TCAGATGCTG GATTATACCA TCATTGCGCA TGAGAGTTTT GAAATCATCC GTCATTCTGT 720

CTACCAGACA GATGATCGTG AAGTGGAAAA TGCTCTGGCT TTTGAAGTGA AAAATGATGA 780

AACAGACAAG CTGATTCTGT TATTAAGCGA GGATATTGGT GTAGGTGAAA AATTGTGCCT 840

CGTTGACGGA ACAAAAATGC GTGGAAAATG TTTAGTATAT GATAAAATAA ATGAGAGAAT 900

GATTCGCTTG CAGTGCTAGA AATAGGCATT TTGAATAGTG AATATGTTAT AATAAGTATT 960

AGTAGGAGGT GTTTTAGATT GGAGAAGAAA CTGACCATAA AAGACATTGC GGAAATGGCT 1020

CAGACCTCGA AAACAACCGT GTCATTTTAC CTAAACGGGA AATATGAAAA AATGTCCCAA 1080

GAGACACGTG AAAAGATTGA AAAAGTTATT CATGAAACAA ATTACAAACC GAGCATTGTT 1140

GCGCGTAGCT TAAACTCCAA ACGAACAAAA TTAATCGGTG TTTTGATTGG TGATATTACC 1200

AACAGTTTCT CAAACCAAAT TGTTAAGGGA ATTGAGGATA TCGCCAGCCA GAATGGCTAC 1260

CAGGTAATGA TAGGAAATAG TAATTACAGC CAAGAGAGTG AGGACCGGTA TATTGAAAGC 1320
ATGCTTCTCT TGGGAGTAGA CGGCTTTATT ATTCAGCCGA CCTCTAATTT CCGAAAATAT 1380
TCTCGTATCA TCGATGAGAA AAAGAAGAAA ATGGTCTTTT TTGATAGTCA GCTCTATGAA 1440
CACCGGACTA GCTGGGTTAA AACCAATAAC TATGATGCCG TTTATGACAT GACCCAGTCC 1500
TGTATCGAAA AAGGTTATGA ACATTTTCTC TTGATTACAG CGGATACGAG TCGTTTGAGT 1560
ACTCGGATTG AGCGGGCAAG TGGTTTTGTG GATGCTTTAA CAGATGCTAA TATGCGTCAC 1620
GCCAGTCTAA CCATTGAAGA TAAGCATACG AATTTGGAAC AAATTAAGGA ATTTTTACAA 1680
AAAGAAATCG ATCCCGATGA AAAAACTCTG GTATTTATCC CTAACTGTTG GGCCCTACCT 1740
CTAGTCTTTA CCGTTATCAA AGAGTTGAAT TATAACTTGC CACAAGTTGG GTTGATTGGT 1800
TTTGACAATA CGGAGTGGAC TTGCTTTTCT TCTCCAAGTG TTTCGACGCT GGTTCAGCCC 1860
TCCTTTGAGG AAGGACAACA GGCTACAAAG ATTTTGATTG ACCAGATTGA AGGTCGCAAT 1920
CAAGAAGAAA GGCAACAAGT CTTGGATTGT AGTGTGAATT GGAAAGAGTC GACTTTCTAA 1980
AATGAAGGAA AATGACTTGC AATCTCTGTT AAGAAATAAA ATAATCCCAC CTAGAACAAG 2040
CTAGGTGGGA TTATTTGCCT ATGAAATGAG AAATTATGGG AGCAAGCTCC TAAATCAACT 2100
GTTTTTGATC TACTTCTTTA ACTACTTGAT AAAAGTTATA GAAGTAGGCC AAACTTGAAA 2160
TGATGGTTAC GACTAGGAAT ATTGAAAATT TCCATTGGAC AGGGTTGGTT AAAAGTTGTG 2220
GAAAGGATAT GAGGAGAAAG AAGAGGGCTG CGTTGAGGAC AGGTATCCGT TTTGATTGTA 2280
TTTTCTCAAG TCCTTTATTG AGCGCAGGAA GAAAGAGGAG TAGGAGTAGT AAAACTGTAT 2340
GAGAAATAGC TCCTGAAGTA AGGGCGAAGA AAAGGAAAAT ACTGATAAAA ACATGAATGA 2400
TCAGTAGTCT AGCTAGTGAT TTCATAAGGC ACCTCCTAAT CCTGGTCTTT TTTAGCTCTT 2460
GCAATACGAA GTGAGTCGAC AATATGTATC ATCACTCCGA AAAAGAAAGC TCCCAGTATA 2520
GTTTTAAAAA TATGTTTTGT ATTTAGAAGA GAACTGATAA AATTTGGATT TTCACTTGTT 2580
AGGGTATCAA TGAGTGGAAT TATAAAAAAT ATCACTGTTC CATAAATCGA ACCTGCTTTC 2640
AGACCAGGAT AACGTAACTG TTTCTTTTCT TTTTTCATGA GTTTCCTCCT AATCCTCATC 2700
TTGATTTTTC TTAGTTTTTG CAATGCGACG GGAGATGAGG AACTGTATGC TCGCTCCGAA 2760
GAAAATAGAA CCGAGAATAC TTGATACACC ATTTCTTATA GTGAGAAGAG AATGAAAATA 2820
GTCCTGACCT TCATCTATGA GTATCCTGAG AAGAGGAGTT ATAAAAAACA TCCATAGACC 2880
AAAGAACAAA CCTGCTTTCA GACCTGGGTA GTGTAGTTGC TTGCTTTCTT TCTCATTCAG 2940
CATATCTGGT TCAATGACTG TGATGCCTGT TTTTTTCATT TGGTAGGTGA CATAGCCAGA 3000

```
AGCGATGAGG GCAATCACTA AAATCAGAGG AGGATAGATT AGAGCCACTT CTTGAGGGTA   3060
TTTATAGGCC AGAAGGAGTG GAATAAGATT TCCGAAAATC ATCAGATAAA AGAGGATGAT   3120
AAAGACTTGG TTCCCAATAC TATCGGCCTC ACGCCGTTTG TATTCGTCAA GGGGACCAGA   3180
AATACCGTAT GTGCGTTTGA TCAGTTTTTC AGTGAAGGTT TCTTTTTTCA TGAGTTTGCT   3240
CCTTTTTTAA AAATCTTCCT CCCAAAAGAG ACTGTTGAGG TCAGTTTGGA GGCTGCGGGC   3300
GAGATTGAGA CAGAGTTCCA AGGTTGGATT GTACTTGTCG TTTTCAATCA TATTGATAGT   3360
CTGTCTCGAG ACACCGATAT CCTTGGCGAG TTCGAGCTGG GAAATACCCA ATTCCTTGCG   3420
AAATTCTTTC ACACGATTCA TCTGTTCTCC TTTCTGATTT ATGTCGTATA TATTTGACTA   3480
TATTATAGTC TTTTAAACAT AAAGTGTCAA GTATTTTTGA CATATTTTTT GAAGAAATAG   3540
TAGTCTCCTT GTCCTATTTG TCTGACAAGT GCAAGCTGGT CGGATTTGTG GTAAAATAGA   3600
TAAGATATGA CAAAAGAATT TCATCATGTA ACGGTCTTAC TCCACGAAAC GATTGATATG   3660
CTTGACGTAA AGCCTGATGG TATCTACGTT GATGCGACTT TGGGCGGAGC AGGACATAGC   3720
GAGTATTTAT TAAGTAAATT AAGTGAAAAA GGCCATCTCT ATGCCTTTGA CCAGGATCAG   3780
AATGCCATTG ACAATGCGCA AAAACGCTTG GCACCTTACA TTGAGAAGGG AATGGTGACC   3840
TTTATCAAGG ACAACTTCCG TCATTTACAG GCATGTTTGC GCGAAGCTGG TGTTCAGGAA   3900
ATTGATGGAA TTTGTTATGA CTTGGGAGTG TCTAGTCCTC AATTAGACCA GCGTGAGCGT   3960
GGTTTTTCTT ATAAAAAGGA TGCGCCACTG GACATGCGGA TGAATCAGGA TGCTAGCCTG   4020
ACAGCCTATG AAGTGGTGAA CAATTATGAC TATCATGACT TGGTTCGTAT TTTCTTCAAG   4080
TATGGAGAGG ACAAATTCTC TAAACAGATT GCGCGTAAGA TTGAGCAAGC GCGTGAAGTG   4140
AAGCCGATTG AGACAACGAC TGAGTTAGCA GAGATTATCA AGTTGGTCAA ACCTGCCAAG   4200
GAACTCAAGA AGAAGGGGCA TCCTGCTAAG CAGATTTTCC AGGCTATTCG AATTGAAGTC   4260
AATGATGAAC TGGGAGCGGC AGATGAGTCC ATCCAGCAGG CTATGGATAT GTTGGCTCTG   4320
GATGGTAGAA TTTCAGTGAT TACCTTTCAT TCCTTAGAAG ACCGCTTGAC CAAGCAATTG   4380
TTCAAGGAAG CTTCAACAGT TGAAGTTCCA AAAGGCTTGC CTTTCATCCC AGATGATCTC   4440
AAGCCCAAGA TGGAATTGGT GTCCCGTAAG CCAATCTTGC CAAGTGCGGA AGAGTTAGAA   4500
GCCAATAACC GCTCGCACTC AGCCAAGTTG CGCGTGGTCA GAAAAATTCA CAAGTAAGAG   4560
GGAAAAAGAT GGCAGAAAAA ATGGAAAAAA CAGGTCAAAT ACTACAGATG CAACTTAAAC   4620
GGTTTTCGCG TGTGGAAAAA GCTTTTTACT TTTCCATTGC TGTAACCACT CTTATTGTAG   4680
CCATTAGTAT TATTTTTATG CAGACCAAGC TCTTGCAAGT GCAGAATGAT TTGACAAAAA   4740
TCAATGCGCA GATAGAGGAA AAGAAGACCG AATTGGACGA TGCCAAGCAA GAGGTCAATG   4800
```

AACTATTACG TGCAGAACGT TTGAAAGAAA TTGCCAATTC ACACGATTTG CAATTAAACA 4860
ATGAAAATAT TAGAATAGCG GAGTAAGATA TGAAGTGGAC AAAAAGAGTA ATCCGTTATG 4920
CGACCAAAAA TCGGAAATCG CCGGCTGAAA ACAGACGCAG AGTTGGAAAA AGTCTGAGTT 4980
TATTATCTGT CTTTGTTTTT GCCATTTTTT TAGTCAATTT TGCGGTCATT ATTGGGACAG 5040
GCACTCGCTT TGGAACAGAT TTAGCGAAGG AAGCTAAGAA GGTTCATCAA ACCACCCGTA 5100
CAGTTCCTGC CAAACGTGGG ACTATTTATG ACCGAAATGG AGTCCCGATT GCTGAGGATG 5160
CAACCTCCTA TAATGTCTAT GCGGTCATTG ATGAGAACTA TAAGTCAGCA ACGGGTAAGA 5220
TTCTTTACGT AGAAAAAACA CAATTTAACA AGGTTGCAGA GGTCTTTCAT AAGTATCTGG 5280
ACATGGAAGA ATCCTATGTA AGAGAGCAAC TCTCGCAACC TAATCTCAAG CAAGTTTCCT 5340
TTGGAGCAAA GGGAAATGGG ATTACCTATG CCAATATGAT GTCTATCAAA AAAGAATTGG 5400
AAGCTGCAGA GGTCAAGGGG ATTGATTTTA CAACCAGTCC CAATCGTAGT TACCCAAACG 5460
GACAATTTGC TTCTAGTTTT ATCGGTCTAG CTCAGCTCCA TGAAAATGAA GATGGAAGCA 5520
AGAGCTTGCT GGGAACCTCT GGAATGGAGA GTTCCTTGAA CAGTATTCTT GCAGGGACAG 5580
ACGGCATTAT TACCTATGAA AAGGATCGTC TGGGTAATAT TGTACCCGGA ACAGAACAAG 5640
TTTCCCAACG AACGATGGAC GGTAAGGATG TTTATACAAC CATTTCCAGC CCCCTCCAGT 5700
CCTTTATGGA AACCCAGATG GATGCTTTTC AAGAGAAGGT AAAAGGAAAG TACATGACAG 5760
CGACTTTGGT CAGTGCTAAA ACAGGGGAAA TTCTGGCAAC AACGCAACGA CCGACCTTTG 5820
ATGCAGATAC AAAAGAAGGC ATTACAGAGG ACTTTGTTTG GCGTGATATC CTTTACCAAA 5880
GTAACTATGA GCCAGGTTCC ACTATGAAAG TGATGATGTT GGCTGCTGCT ATTGATAATA 5940
ATACCTTTCC AGGAGGAGAA GTCTTTAATA GTAGTGAGTT AAAAATTGCA GATGCCACGA 6000
TTCGAGATTG GGACGTTAAT GAAGGATTGA CTGGTGGCAG AACGATGACT TTTTCTCAAG 6060
GTTTTGCACA CTCAAGTAAC GTTGGGATGA CCCTCCTTGA GCAAAAGATG GGAGATGCTA 6120
CCTGGCTTGA TTATCTTAAT CGTTTTAAAT TTGGAGTTCC GACCCGTTTC GGTTTGACGG 6180
ATGAGTATGC TGGTCAGCTT CCTGCGGATA ATATTGTCAA CATTGCGCAA AGCTCATTTG 6240
GACAAGGGAT TTCAGTGACC CAGACGCAAA TGATTCGTGC CTTTACAGCT ATTGCTAATG 6300
ACGGTGTCAT GCTGGAGCCT AAATTTATTA GTGCCATTTA TGATCCAAAT GATCAAACTG 6360
CTCGGAAATC TCAAAAAGAA ATTGTGGGAA ATCCTGTTTC TAAAGATGCA GCTAGTCTAA 6420
CTCGGACTAA CATGGTTTTG GTAGGGACGG ATCCGGTTTA TGGAACCATG TATAACCACA 6480
GCACAGGCAA GCCAACTGTA ACTGTTCCTG GGCAAAATGT AGCCCTCAAG TCTGGTACGG 6540

```
CTCAGATTGC TGACGAGAAA AATGGTGGTT ATCTAGTCGG GTTAACCGAC TATATTTTCT    6600
CGGCTGTATC GATGAGTCCG GCTGAAAATC CTGATTTTAT CTTGTATGTG ACGGTCCAAC    6660
AACCTGAACA TTATTCAGGT ATTCAGTTGG GAGAATTTGC CAATCCTATC TTGGAGCGGG    6720
CTTCAGCTAT GAAAGACTCT CTCAATCTTC AAACAACAGC TAAGGCTTTA GAGCAAGTAA    6780
GTCAACAAAG TCCTTATCCT ATGCCTAGTG TCAAGGATAT TTCACCTGGT GATTTAGCAG    6840
AAGAATTGCG TCGCAATCTT GTACAACCCA TCGTTGTGGG AACAGGAACG AAGATTAAAA    6900
ACAGTTCTGC TGAAGAAGGG AAGAATCTTG CCCCGAACCA GCAAGTCCTT ATCTTATCTG    6960
ATAAAGCAGA GGAGGTTCCA GATATGTATG GTTGGACAAA GGAGACTGCT GAGACCCTTG    7020
CTAAGTGGCT CAATATAGAA CTTGAATTTC AAGGTTCGGG CTCTACTGTG CAGAAGCAAG    7080
ATGTTCGTGC TAACACAGCT ATCAAGGACA TTAAAAAAAT TACATTAACT TTAGGAGACT    7140
AATATGTTTA TTTCCATCAG TGCTGGAATT GTGACATTTT TACTAACTTT AGTAGAAATT    7200
CCGGCCTTTA TCCAATTTTA TAGAAAGGCG CAAATTACAG GCCAGCAGAT GCATGAGGAT    7260
GTCAAACAGC ATCAGGCAAA AGCTGGGACT CCTACAATGG GAGGTTTGGT TTTCTTGATT    7320
ACTTCTGTTT TGGTTGCTTT CTTTTTCGCC CTATTTAGTA GCCAATTCAG CAATAATGTG    7380
GGAATGATTT TGTTCATCTT GGTCTTGTAT GGCTTGGTCG GATTTTTAGA TGACTTTCTC    7440
AAGGTCTTTC GTAAAATCAA TGAGGGGCTT AATCCTAAGC AAAAATTAGC TCTTCAGCTT    7500
CTAGGTGGAG TTATCTTCTA TCTTTTCTAT GAGCGCGGTG GCGATATCCT GTCTGTCTTT    7560
GGTTATCCAG TTCATTTGGG ATTTTTCTAT ATTTTCTTCG CTCTTTTCTG GCTAGTCGGT    7620
TTTTCAAACG CAGTAAACTT GACAGACGGT GTTGACGGTT TAGCTAGTAT TTCCGTTGTG    7680
ATTAGTTTGT CTGCCTATGG AGTTATTGCC TATGTGCAAG GTCAGATGGA TATTCTTCTA    7740
GTGATTCTTG CCATGATTGG TGGTTTGCTC GGTTTCTTCA TCTTTAACCA TAAGCCTGCC    7800
AAGGTCTTTA TGGGTGATGT GGGAAGTTTG GCCCTAGGTG GGATGCTGGC AGCTATCTCT    7860
ATGGCTCTCC ACCAAGAATG GACTCTCTTG ATTATCGGAA TTGTGTATGT TTTTGAAACA    7920
ACTTCTGTTA TGATGCAAGT CAGTTATTTC AAACTGACAG GTGGTAAACG TATTTTCCGT    7980
ATGACGCCTG TACATCACCA TTTTGAGCTT GGGGGATTGT CTGGTAAAGG AAATCCTTGG    8040
AGCGAGTGGA AGGTTGACTT CTTCTTTTGG GGAGTGGGAC TTCTAGCAAG TCTCCTGACC    8100
CTAGCAATTT TATATTTGAT GTAAGAATGG CACCCTGATG TTTCAGGG                 8148
```

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9909 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```
TACTCCACCC TTAATATCCG TTCCTGTAAA TACTTTACCG CTTTTAAGTT CATAGAATTG      60
AACTTTTAAA TGCTTGTCTT CAAGCATCTT TTCCATCCAA TTTTTAGGAG TTTGACCAGC     120
TTTAAATAAA AACCTTGCTG GGGTGATTAG TATAGATTTA TCTGCGATTT TATAAGCTTC     180
ATCAATAAAA TAGTGATATA TCGGCTCATC TCTGGCTTCT CCTGTTTCCT GATACGGAGG     240
ATTTCCTATC ACGACATCAA ATTTCATTTC ACTTTCCTCG CTAGATAGGC GCTCAAAACC     300
TATCATTCTA TTCTTTTTCC AGTCTTTGAT ATGGGTTTTA GATTCTTCTA CTTCTTGGAC     360
TTCTAGCTCA TCCGCAAACA AACTCAATTG TTGAGATTGC TTTTGTTTAG CTGAATAAGG     420
ACTACTTTTT TTCAATCCAT CCATCTGAAA GACATTGTAA GAGATAATAG TCGCAATTTC     480
TTTCTTTTGC TCTAATGTTG GTTGATTTCC AGTCTTAGCT AGATAATAGT CCTCAAAAGT     540
TGCCAAAAGA TTCTCACGCG CCAAAAGGAG AGAATCTCCT TGATACTCAT AACCATACGA     600
AGCATGATAA GCATCTTTTA CAAGTTTATA AAATGTGACT TCATCTGAAA CCTCACGACT     660
AATCCGTTGC AGTTTTCTAT CAACAAAACC AACTCGCTCA GATAATGGAA TTTCCTCACC     720
AGTTACGGTA TCATATCTCG TTACCATATA AGGTGCTTCA CCACAAGTTA CCTCTAACCA     780
TCGTAAGTCC ACATACTCCT CAAGACTTAA CGAGCCTAAT TTCGATTCTA CATATCCATT     840
TTGCTTTGCG ACCAACCACG TTGGTGTAAA CACTTCTGCC CTTATTTTTG TCCGATCTTT     900
TTGTTCATAT TTGGATTTTT CAGATCTGGG CTGAATCAAG TTGGCAAAGT TTCCAGTAAC     960
CTTACTTGGA TTGATGCGAT CACTTGGAGC AAATCCCTTT CCTAACAATT CATAAGAATG    1020
CGTAnGCCAA ACAATTGATT TCTTTGTCGT TCGATCTTTT AAAAGAATTT TTAATAAGTC    1080
AGCCGATTCT TTAGCCAAAC TTTCTTCACT AATATCTATT GTCATCAGCA ACCTCTCTTA    1140
TATTGTAAGC CCTATTATAT CATATTTTAA AGAATGAAAA TTTACTTGAA AAAAGTAATT    1200
CAATAAATAT CTCTCCGATG ACCAACTTCT AGAGTAGCAA CGACTAATTC ATCATCTACA    1260
ATTTGTACGA TAACTCGATA ATTACCAATT CTATAGCGCC ATTGACCAAC GCGATTACCA    1320
ACCAAAGCCT TTCCGTGTCG TCTTGGGTCT TCCAAAACAT TGGTTTGTAA ATAGTTTGTA    1380
ATTAGCTTCT GCGTATAACG GTCCAATTTT TTCAATTGCT TGATAAAACG TCTTGTTGGA    1440
ACTAATTTAT ACAAATTATT CATCCTTCAA GCCTAAATCA TGCATCATTT CTTCCCAAGT    1500
AATGGGTTCA ACTCCTTTTT CCAAGTCTTC TAAATACTCT TGATAGGCTA AATCTGCCAC    1560
```

```
ACGAGCATCG TATTCATCTT CTAGGGCTTC AAGAGTTTTG GTGCGAATAA GTTCCGAAAG 1620
GGAAACTCCT TCAAACTTAG CCATTGCTTT CATAAATGTT TTATCAGCTT CAGAAACTTT 1680
TAATGTAATA GTAGTCATCT TTTGTGCTCC CTTTTTTAAT GGTAACACCA TTGTATTACT 1740
TTTTAGGTGT TCAGTCAATA TAAAAAGAAC ACCTTCTCAG CGTTCTTTCT ATATCTCTGT 1800
CAATGGTGTT GCGGTATCTG GTGAGGTATC ATAAACCTTA AAGTCTACTC CGACTCCCAG 1860
ATCAGCTTGA GCCAGCTGAT TGACCATGGT CATATGAGCC AGTTCCTTGA TATTGTTTTC 1920
CTTAGATAAA TGCCCAAGGT AAATCTTCTT AGTACGATTT CCTAGCGTCC GAATCATAGC 1980
TTCAGCACCG TCCTCGTTAG AAAGGTGACC AAGGTCAGAT AGGATTCGTT GTTTGAGTCG 2040
CCAAGCGTAA GAACCTGATC GCAAAATCTC TACATCATGG TTGGCCTCGA TAAGATAACC 2100
ATCCGCATTT TCGACAATGC CCGCCATACG GTCACTGACA TAACCTGTAT CTGTCAAGAG 2160
GACAAAACTC TTATCATCCT TCATAAAGCG ATAGAACTGC GGTGCGACTG CATCATGGCT 2220
TACACCAAAA CTCTCGATGT CGATATCTCC AAAGGTTTTG GTTTTACCCA TTTCAAAAAT 2280
ATGCTTTTGC GAAGAATCCA CCTTGCCAAG ATATTTACTA TTTTCCATAG CTTGCCAGGT 2340
CTTTTCATTG GCATAAAGAT CCATACCATA CTTGCGAGCC AAAACGCCTA CTCCATGGAT 2400
ATGATCTGAA TGCTCATGGG TAATCAAGAT GGCATCCAGG TCTTCTGGCT TACGGTTAAT 2460
TTCAGCTAGC AGACTGGTAA TTTTCTTGCC AGACAAGCCT GCATCTACTA AAAGCTTCTT 2520
TTTTGAGGTT TCCAGATAAA AAGAATTTCC ACTGGAACCC GACGCTAAAA TACTGTATTT 2580
AAAGCCTATT TCACTCATTC TAGTCTTCTA CTTCATCCTC CCATACTTCT TCTTTCACTG 2640
CATCCTTATC ATAAGGGAGT ACAATGGTAA AGGTTGAACC CTTGCCGTAT TCACTCTTGG 2700
CCCAAATAAA GCCCTTATGT TGTTTGATAA TTTCTTTAGC GATAGACAGT CCTAGACCTG 2760
TACCACCTTG TGCACGACTT CTAGCACGAT CCACACGATA GAAACGGTCA AAGATACGTG 2820
GTAAATCCTG CTTAGGAATC CCCAAACCGT GGTCAGAAAT GGATAAAATC ATCTGGTCTT 2880
CAGTTGTCTT CATTCTGACA GTGATTTTAC CCCCATCTGG CGAATACTTA ATAGCATTAT 2940
TTAAAATATT GTCGACAACC TGCGTCATCT TATCTGTATC AATTTCCATC CAGATAGAAT 3000
TGATGGGATA ATCTCTCACC AACTCATATT TTTTCTCCTT TTCCTGTCCT TTCATCTTGT 3060
CAAAACGATT GAGGATAAAG GTAATAAAAG CAGTGAAGTT AATCAGTTCC ACATCTAGGT 3120
GACTGGTAGC ATTATCAATA CGTGAAAGAT GGAGGAGATC CGTCACCATG CGCATCATAC 3180
GGTTGGTCTC ATCAAGAGAA ACCTTGATAA AGTCTGGTGC TACAGTTTCA CACAAAGCCC 3240
CCTCATCCAA GGCTTCAAGA TAGGATTTTA CGCTAGTCAG AGGAGTCCGT AACTCATGGC 3300
TAACATTGGA AACAAAGAGT CTTCGTTCGC GTTCTTCCTT CTCCTGCTCC GTCGTATCAT 3360
```

GCAAAACAGC CACCAAACCT GAAATAAAGC CAGACTCTCG ACGTATCAAG GCAAAGCGAA 3420
CTCGAAGGTT CAAATATTCG CCATTGATAT CTTGGGAATC TAGCAACAAT TCTGGACTTT 3480
GGGTAATCAA ATCACGCAAT TCATAGTTTT CTTCTATCTT GAGCAATTCC AAAATGCTTC 3540
TATTCAGAAC ATCTTCCTTA ACCAACCCCA GTTGCTTCTT GGCTGTATCG TTAATCATGA 3600
TAATCTGACC CCGACGGTTA GTCGCAAGAA CCCCATCTGT CATATAAAAC AGAATACTAT 3660
TTAGCCTCTT ACTCTCTTGT TCTAGATTTT CCTGAGTGAG ACGAATAACC TCCGACAAGT 3720
CATTCAAATT ATTGGTAATA TTGGTGATTT CAGACCCACC TTGCATATCA AGAACCTTGG 3780
AATAATCTCC TGCAATCAAA TCTTTAACCT TTTGATTGAC TTGCTTCAAC TGAATATTAT 3840
CACGTCTATT TTCCAGTAAT AAGAGGGTCA CAACAAGGAT GAAACCTAAC AAAATCAGGA 3900
TAAAGATAAA ATCTCTGGTA AAAATGGTTT GTTTCAGTAA ATCAAGCATT ATTTCTCATG 3960
TAATACCCTA CACCACGGCG CGTCAAGATA TACTCTGGTC GGCTGGGCGT ATCTTCAATC 4020
TTCTCACGCA GACGTCGTAC AGTCACATCA ACTGTACGGA CATCACCAAA ATAGTCATAA 4080
CCCCAGACAG TCTCAAGCAA GTGTTCGCGC GTGATGACTT GACCTGTATG CGATGCTAAA 4140
TGATACAAAA GCTCAAATTC ACGATGGGTT AAGTCTAGTT CTTCGCCATA TTTTTAGCC 4200
ACGTAGGCGT CTGGAACAAT TTCTAAATCC CCAATTTGGA TAGGTTGAGG TTTACTATCT 4260
GCTTCCTGAC CATCTACTGG CATAGGTTGA GAACGACGCA GAAGAGCTTT AACACGCGCC 4320
TGCAACTCAC GATTGGAGAA GGGTTTTGTT ACATAGTCAT CTGCCCCAAG TTCCAAACCG 4380
ATAACCTTAT CAAATTCACT ATCTTTGGCT GAAAGCATAA GAATGGGCAC ACTGCTTGTC 4440
TTACGAATGG TCTTAGCAAC TTCTAAACCA TCAATTTCTG GAAGCATCAA ATCCAGAATA 4500
ATAATATCTG GTTGCTCTGC TTCAAATTGC TCTAGCGCTT CACGACCATT AAAAGCAGTT 4560
ACAACTTCGT AACCTTCCTT GGTCATATTA AACTTGATAA TATCCGAGAT TGGTTTCTCA 4620
TCATCTACAA TTAGTATTTT TTTCATATGT TCACCTTTTT CTCTACTATT ATACCAAAAA 4680
AATAGTCAGA AGACACAATA GCTAGTCTTG GCTACTGTCT AAGTTGGCTT GTGCATAAAC 4740
CTGCCAGATT TTTTGTTGGG GTTTGGCAAG TGGGTAATTC TTGAATTCTT CTGGTGAAAG 4800
CCAGCGAACT TCCCTATCTG AAAAATCATG GAAGTCACTC ACCTGACCTG CTACAATCTG 4860
TACATGCCAT TTTCGATGAC TAAAAACATG CTGGACTGTA TCAAAACAAA CATCAAGCCA 4920
ATCAACATCT AGGTCATAGT CCTGCTGGAA ACTCTCTTCT GGACTGGGAC CAAAGTTCAC 4980
ACTTTCTTCC GCAACCTGAT GAAAGAGGTC AAACTGCTCT TCTTGCGAAA AGTTATCAAC 5040
TTCTATAAAG GGGAAATGCC AAAAACCTGC CAAGAGCTTT TCGCTTTCAT TTTTTTCAAG 5100

TAAAAATTGT CCTTGAGAAT TTTTCACAAC TAAGGCTTTA AGATAAATAG GAACCGGCTT 5160

TTTCTTAGGA GATTTAATTG GATAACGGTC CATGGTTCCA TTCTGATATG CCGCACTAAA 5220

GTCCTTGACT GGGCTTTCTT CAGGTCTGGG ATTTACAGGA GACTCAATAT CAGACCCTAA 5280

GTCCATCAAG GCTTGATTAA AATCACCCGG ACGATCCGGA TTAATCAAGA TCTCCATCAT 5340

TGCCTGAAAA ATTTTTCGAT TACTTGGAAT CCCAATATCG TGGTTGACTT CAAACAGACG 5400

CGCCAAGACC CGCATGACAT TACCATCTAC AGCTGGCTCA GGCAAGTTAA AAGCAATACT 5460

GGAAATGGCT CCTGCTGTGT AAGGTCCAAT CCCTTTCAAG CTGGAAATTC CTTCATAGGT 5520

ATTTGGAAAT TGGCCACCAA AGTCAGTCAT AATCTGCTGG GCTGCAGCCT GCATATTGCG 5580

AACTCGAGAA TAATAGCCCA AGCCCTCCCA AGCTTTCAGT AAACTCTCCT CAGGCGCAGT 5640

TGCCAGACTT TCGACAGTTG GAAACCAGTC CAAAAATCTT TCGTAGTAAG GGATAACTGT 5700

ATCCACCCTG GTCTGCTGAA GCATGATTTC AGATACCCAG ATGTGATAAG GATTTTTACT 5760

TCTCCTCCAA GGCAAATCTC TTTTGTTTTC ATCATACCAA GCGAGAAGTT TCTCACGGAA 5820

AGAAATGACT TTCTCCTCCG GCCACATGAC GATACCGTAT TCTTTCAAAT CTAACATATC 5880

TCTAGTATAA CACAGAAGGT TTCACCTGTC TTTGTATCTG ATTTATAATA TTTTCAATAG 5940

ATAGTATATA ACTTTTCTAT CTACTTATAC TCAATGAAAA TCAAAGAGCA AACTAGGAAG 6000

CTAGCCGCAG GTTGCTCAAA ACACTGTTTT GAGGTTGTGG ATAGAACTGA CAGAGTCAGT 6060

ATCATATAcT ACGGCAAGGT GAAGCTGACG TAGTTTGAAG AGATTTTCGA AGAGTATAAA 6120

TCTTATTGAT GAACTGCTTG CAGTCTGAGA AAAAATGAGC TTGGATATTA TTTCCAAACT 6180

CACTTAAAGT CAATTTCAAT CCACTAGAAC AAGCCTAGTA CAGTTCCATC GCTTTCAACA 6240

TCCATGTTGA GAGCTGCTGG ACGTTTTGGA AGACCTGGCA TGGTCATAAC ATCACCAGTT 6300

AAGGCAACGA TGAAGCCTGC ACCTAATTTT GGTACCAATT CACGAATGGT AATTTCAAAG 6360

TTTTCTGGTG CTCCAAGCGC ATTTGGATTG TCTGAGAAAC TGTATTGAGT TTTAGCCATA 6420

CAGATTGGCA ATTTGTCCCA ACCGTTTTGA ACGATTTGAG CAATTTGTGT TTGAGCTTTC 6480

TTCTCAAAGT TCACTTTGCT ACCACGATAG ATTTCAGTGA CAATTTTTTC AATCTTTTCT 6540

TGGACAGAAA GGTCATTATC ATACAAACGT TTATAGTTAG CTGGATTTTC AGCAATTGTC 6600

TTAACAACTG TTTCGGCAAG TGCTACTCCA CCTTCTGCTC CATCAGCCCA GACACTAGCC 6660

AATTCAACTG GTACATCGAT TGAGGCACAG AGTTCTTTTA AGGCTGCAAT TTCAGCTTCT 6720

GTATCAGATA CAAATTCGTT AATAGCTACA ACTGCTGGAA TACCGAACTT ACGGATATTT 6780

TCAACGTGGC GTTTCAAGTT AGCAAAACCT GCACGAACTG CCTCTACATT TTCTTCAGTC 6840

AGAGCGTCTT TAGCCACACC ACCATTCATC TTAAGGGCAC GAAGGGTTGC GACAATAACA 6900

ACTGCATCTG GAGATGTTGG CAAGTTTGGT GTCTTGATAT CAAGGAATTT CTCAGCACCA 6960
AGGTCCGCAC CAAAACCAGC TTCAGTAACA GTGTAATCAG CCAAGTGAAG GGCTGTTGTC 7020
GTCGCCAAAA CAGAGTTACA GCCATGAGCG ATATTGGCAA ATGGACCACC GTGTACAAAG 7080
GCAGGTGTAC CGTAAATTGT CTGAACCAAG TTTGGCTTAA TAGCATCCTT CAAAATCAAA 7140
GCCAAGGCAC CCTCAACCTG CAAATCACCT ACAGAAACAG GCGTACGGTC ATAGCGATAA 7200
CCAATAACGA TATTCGCCAA ACGACGTTTC AAGTCCTCGA TGTCCGTTGC CAAGCAAAGA 7260
ATTGCCATGA TTTCTGAAGC AACTGTAATA TCAAAACCAT CCTCACGTGG AATACCGTTT 7320
AGAGGACCAC CAAGACCAAC AGTCACATGG CGGAGCGTAC GGTCGTTCAA GTCCACAACG 7380
CGTTTCCAGA GGATACGACG TTGATCAATT CCCAGCTCAT TCCCTTGGTG CAAGTGGTTG 7440
TCAATCAAGG CAGAAAGGGC ATTGTTGGCA GTTGTAATAG CATGCATATC TCCAGTAAAG 7500
TGGAGGTTGA TGTCTTCCAT TGGCAGAACT TGTGCATACC CACCACCAGC AGCACCACCC 7560
TTGATCCCCA TGACTGGACC AAGAGACGGT TCGCGGATAG CAATCATGGT TTTCTTGCCA 7620
ATCTTGTTCA AGGCATCCGC AAGACCAATG GTAAGCGTCG ACTTTCCTTC ACCTGCAGGT 7680
GTTGGGTTGA TGGCAGTAAC CAAGATCAAT TTACCGACTG GATTGCTCTC AACTGCACGA 7740
ATTTTATCAA AGCTGAGTTT AGCCTTGTAC TTTCCGTACA ACTCCAAATC GTCATAAGAA 7800
ATACCAAGTT TCTCTACAAC ATCAACAATT GGCTTCAACT CAATACTCTG TGCGATTTCA 7860
ATATCTGTTT TCATTCAAAA TTCCTCTAAC CTCTTATATG ATAATTCATT ATATCACAAA 7920
ACAAGATTTT TAACATCCTA AAACTCTCTA AACGTTCGTA AATATCTCTG TTTTTAAGAC 7980
TTTTAGAGTC CTTTCTTAAA TTTTATATGG CTTTATAGTT TGAAACTATA ATAAATCTTC 8040
GTTTTTACCA AAAATTTATC ACTTTCATTT TACTTACCGC TTATTTTTGT GTACAATAGT 8100
GCTATGAAAA TTTTAGTTAC ATCGGGCGGT ACCAGTGAAG CTATCGATAG CGTCCGCTCT 8160
ATCACTAACC ATTCTACAGG TCACTTGGGG AAAATTATCA CAGAGACTTT GCTTTCTGCA 8220
GGGTATGAAG TTTGTTTAAT TACGACAAAA CGAGCTCTGA AGCCAGAGCC TCATCCTAAC 8280
CTAAGTATTC GAGAAATTAC CAATACCAAG GACCTTCTAA TAGAAATGCA AGAACGTGTT 8340
CAGGATTATC AGGTCTTGAT CCACTCAATG GCTGTTTCTG ACTACACTCC TGTTTATATG 8400
ACAGGGCTTG AGGAAGTTCA GGCTAGCTCC AATCTAAAAG AATTTTTAAG CAAGCAAAAT 8460
CATCAGGCCA AGATTTCTTC AACTGATGAG GTTCAGGTTT TGTTCCTTAA AAAGACACCC 8520
AAAATCATAT CCCTAGTCAA GGAATGGAAT CCTACTATTC ATCTGATTGG TTTCAAACTG 8580
CTGGTTGATG TTACCGAAGA TCATCTGGTT GACATTGCAC GAAAAAGTCT TATCAAGAAT 8640

```
CAAGCAGATT TAATCATCGC GAATGACCTG ACTCAAATTT CAGCAGATCA GCACCGAGCT    8700
ATATTTGTTG AGAAAAATCA GCTTCAAACA GTCCAGACTA AAGAAGAAAT TGCAGAACTC    8760
CTCCTTGAAA AAATTCAAGC CTATCATTCT TAGAAAGGAA AACTATGGCA AACATTCTCT    8820
TGGCTGTAAC GGGTTCAATC GCCTCTTATA AGTCGGCAGA TTTAGTCAGT TCTCTAAAAA    8880
AACAAGGCCA TCAAGTCACT GTCTTAATGA CTCAGGCTGC TACAGAGTTT ATCCAACCTT    8940
TGACACTACA GGTACTCTCA CAGAATCCTG TCCACTTGGA TGTCATGAAG GAACCCTATC    9000
CTGATCAGGT CAATCATATC GAACTTGGAA AAAAAGCAGA TTTATTTATC GTGGTACCTG    9060
CAACTGCTAA CACTATTGCA AAACTAGCTC ACGGATTTGC GGACAACATG GTAACCAGTA    9120
CAGCTCTAGC CCTACCAAGT CATATTCCCA AACTAATAGC TCCTGCTATG AATACAAAAA    9180
TGTATGACCA TCCAGTAACT CAGAATAATC TGAAAACATT AGAAACTACG GCTATCAGCT    9240
GATTGCTCCT AAGGAATCCC TACTAGCTTG TGGAGACCAC GGACGAGGAG CTTTAGCTGA    9300
CCTCACAATT ATTTTAGAAA GAATAAAGGA AACTATCGAT GAAAAAACGC TCTAATATTG    9360
CACCCATTGC TATCTTTTTT GCTACCATGC TCGTGATACA CTTTCTGAGC TCACTTATCT    9420
TTAACCTTTT TCCATTTCCA ATCAAACCGA CCATTGTTCA TATTCCTGTC ATTATTGCCA    9480
GCATTATTTA TGGTCCACGA GTTGGGGTTA CACTTGGATT TTTGATGGGA TTACTTAGCT    9540
TGACGGTTAA CACGATTACG ATTCTACCGA CAAGCTACCT CTTCTCTCCC TTCGTACCAA    9600
ACGGAAACAT CTACTCAGCT ATCATTGCCA TCGTCCCACG TATTTTGATT GGTTTAACTC    9660
CTTACTTAGT CTATAAACTG ATGAAAAACA AGACTGGTCT GATTTTAGCT GGAGCCCTTG    9720
GTTCcTTGAC AAATACTATC TTTGTCCTTG GAGGAATCTT CTTCCTATTT GGAAATGTTT    9780
ATAATGGAAA TATCCAACTT CTTCTGGCAA CCGTTATCTC AACAAATTCA ATTGCTGAAT    9840
TGGTCATTTC TGCAATTCTA ACCCTAGCCA TTGTTCCACG ACTACAAACC TTGAAAAAAT    9900
AAAAACAGG                                                            9909
```

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```
TAATTTTCAT ATAATAGTAA AATAGAATGT GTGATTCAAT AATCACCTCA AATAGAAAGG      60
AAATTCTATG TCAAATCTAT CTGTTAATGC AATTCGTTTT CTAGGTATTG ACGCCATTAA     120
```

TAAAGCCAAC TCAGGTCATC CAGGTGTGGT TATGGGAGCG GCTCCGATGG CTTACAGCCT 180

CTTTACAAAA CAACTTCATA TCAATCCAGC TCAACCAAAC TGGATTAACC GCGACCGCTT 240

TATTCTTTCA GCAGGTCATG GTTCAATGCT CCTTTATGCT CTTCTTCACC TTTCTGGTTT 300

TGAAGATGTC AGCATGGATG AGATTAAGAG TTTCCGTCAA TGGGGTTCAA AAACACCAGG 360

TCACCCAGAA TTTGGTCATA CGGCAGGGAT TGATGCTACG ACAGGTCCTC TAGGGCAAGG 420

GATTTCAACT GCTACTGGTT TTGCCCAAGC AGAACGTTTC TTGGCAGCCA AATATAACCG 480

TGAAGGTTAC AATATCTTTG ACCACTATAC TTACGTTATC TGTGGAGACG GAGACTTGAT 540

GGAAGGTGTC TCAAGCGAGG CAGCTTCATA CGCAGGCTTG CAAAAACTTG ATAAGTTGGT 600

TGTTCTTTAT GATTCAAATG ATATCAACTT GGATGGTGAG ACAAAGGATT CCTTTACAGA 660

AAGTGTTCGT GACCGTTACA ATGCCTACGG TTGGCATACT GCCTTGGTTG AAAATGGAAC 720

AGACTTGGAA GCCATCCATG CTGCTATCGA AACAGCAAAA GCTTCAGGCA AGCCATCTTT 780

GATTGAAGTG AAGACGGTTA TTGGATACGG TTCTCCAAAC AAACAAGGAA CTAATGCTGT 840

ACACGGCGCC CCTCTTGGAG CAGATGAAAC TGCATCAACT CGTCAAGCCC TCGGTTGGGA 900

CTACGAACCA TTTGAAATTC CAGAACAAGT ATATGCTGAT TTCAAAGAAC ATGTTGCAGA 960

CCGTGGCGCA TCAGCTTATC AAGCTTGGAC TAAATTAGTT GCAGATTATA AAGAAGCTCA 1020

TCCAGAACTG GCTGCAGAAG TAGAAGCCAT CATCGACGGA CGTGATCCAG TCGAAGTGAC 1080

TCCAGCAGAC TTCCCAGCTT TAGAAAATGG TTTTtCTCAA GCAACT 1126

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2520 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CCGGCAACAA AAAAGAAAAA ATCAACAGTT AAAAAAAATC TAGTCATCGT GGAGTCGCCT 60

GCTAAGCCAA GACGATTGAA AAATATCTAG GCAGAAACTA CAAGGTTTTA GCCAGTGTCG 120

GGCATATCCG TGATTTGAAG AAATCCAGTA TGTCCGTCGA TATTGAAAAT AATTATGAAC 180

CGCAATATAT TAATATCCGA GGAAAAGGCC CTCTTATCAA TGACTTGAAA AAGAAGCTA 240

AAAAAGCTAA TAAAGTTTTT CTCGCGAGTG ACCCGGACCG TGAAGGAGAA GCGATTTCTT 300

GGCATTTGGC CCATATTCTC AACTTGGATG AAAATGATGC CAACCGTGTG GTCTTCAATG 360

AAATCACCAA GGATGCAGTC AAAAATGCTT TTAAAGAACC TCGTAAGATC GATATGGACT 420

TGGTCGATGC CCAACAAGCT CGTCGGATCT TGGATCGCTT GGTAGGGTAT TCGATTTCGC 480

CTATTTTGTG GAAGAAGGTC AAGAAGGGCT TGTCAGCAGG TCGCGTTCAG TCCATTGCCC 540

TTAAACTCAT CATTGACCGT GAAAATGAAA TCAATGCCTT CCAGCCAGAA GAATACTGGA 600

CAGTTGATGC TGTCTTTAAA AAGGGAACCA AACAATTTCA TGCTTCCTTC TATGGAGTAG 660

ATGGTAAAAA GATGAAACTG ACCAGCAATA ACGAAGTCAA GGAAGTCTTG TCTCGTCTGA 720

CGAGTAAAGA CTTTTCAGTA GATCAGGTGG ATAAGAAAGA GCGCAAGCGC AATGCTCCTT 780

TACCCTATAC CACTTCATCT ATGCAGATGG ATGCTGCCAA TAAAATCAAT TTCCGTACTC 840

GAAAAACCAT GATGGTTGCC CAACAGCTCT ATGAAGGAAT TAATATCGGT TCTGGTGTTC 900

AAGGTTTGAT TACCTATATG CGTACCGATT CGACTCGTAT CAGTCCTGTA GCGCAAAATG 960

AGGCGGCAAG CTTCATTACG GATCGTTTTG GTAGCAAGTA TTCTAAGCAC GGTAGCAAGG 1020

TCAAAAACGC ATCAGGTGCT CAGGATGCCC ATGAGGCTAT TCGTCCGTCA AGTGTCTTTA 1080

ATACACCAGA AAGCATCGCT AAGTATCTGG ACAAGGATCA GCTTAAGCTA TATACCCTTA 1140

TCTGGAATCG TTTTGTGGCT AGCCAGATGA CAGCGGCCGT TTTTGATACC ATGGCTGTTA 1200

AATTGTCTCA AAAAGGGGTT CAATTTGCTG CCAATGGTAG TCAGGTTAAG TTTGATGGTT 1260

ATCTTGCCAT TTATAATGAT TCTGACAAGA ATAAGATGTT ACCGGACATG GTTGTTGGAG 1320

ATGTGGTCAA ACAGGTCAAT AGCAAACCAG AGCAACATTT CACCCAACCG CCTGCCCGTT 1380

ATTCTGAAGC AACACTGATT AAAACCTTAG AGGAAAATGG GGTTGGACGT CCATCAACCT 1440

ACGCGCCAAC CATTGAAACC ATTCAGAAAC GTTATTATGT TCGCCTGGCA GCCAAACGTT 1500

TTGAACCGAC AGAGTTGGGA GAAATTGTCA ATAAGCTCAT CGTTGAATAT TTCCCAGATA 1560

TCGTAAACGT GACCTTCACA GCTGAAATGG AAGGTAAACT GGATGATGTC GAAGTTGGAA 1620

AAGAGCAGTG GCGACGGGTC ATTGATGCCT TTTACAAACC ATTCTCTAAA GAAGTTGCCA 1680

AGGCTGAAGA AGAAATGGAA AAAATCCAGA TTAAGGATGA ACCAGCTGGA TTTGACTGTG 1740

AAGTGTGTGG CAGTCCAATG GTCATTAAAC TTGGTCGTTT TGGTAAATTC TACGCTTGTA 1800

GCAATTTCCC AGATTGCCGT CATACCCAAG CAATCGTGAA AGAGATTGGT GTTGAGTGTC 1860

CAAGCTGTCA TCAGGGACAA ATTATTGAGC GAAAAACCAA GCGTAATCGC CTATTCTATG 1920

GTTGCAATCG CTATCCAGAA TGTGAATTTA CCTCTTGGGA CAAGCCTGTT GGTCGTGACT 1980

GTCCAAAATG TGGCAACTTC CTCATGGAGA AAAAAGTCCG TGGTGGTGGC AAGCAGGTTG 2040

TTTGTAGCAA AGGCGACTAC GAGGAAGAAA AGATGGCTCT TTGTCAACTG TAGTGGGTTG 2100

AAGTCAGCTA AGCTCGAGAA AGGACAAATT TTGTCCTTTC TTTTTTGATA TTCAGAGCGA 2160

TAAAAATCCG TTTTTTGAAG TTTTCAAAGT TCCGAAAACC AAAGGCATTG CGCTTGATAA 2220

GTTTGATGAG ATTATTGGTC GCTTCCAATT TGGCGTTAGA ATAGTGTAGT TGAAGGGCGT 2280

TGACGATTTT CTCTTTGTCC TTTAGAAAGG TTTTAAAGAC AGTCTGAAAA AGAGGATGAA 2340

CCTGCTTTAG ATTGTCCTCA ATGAGTCCGA AAAATTTCTC CGGTTCCTTA TTCTGAAAGT 2400

GAAACAGCAA GAGTTGATAG AGCTGATAGT GATGTTTCAA GTCTTGTGAA TAGCTCAAAA 2460

GCTTGTTTAA AATCTCTTTA TTGGTTAAAT GCATACGAAA AGTAGGGCGA TAAAAATGTT 2520

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10993 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TTTTCTCGAT AATAACTTCC ACCTTATTAT TTGGGATACC CTCCTCTTCT TCACCACCAC 60

GTTCATAGTA GTCATCGCGA TAGAGAAAAG CTACGATATC AGCGTCCTGC TCAATAGACC 120

CAGATTCACG AATATCAGAC AAGACCGGTC TCTTGTCCTG ACGTTGTTCT ACACCACGAG 180

AAAGCTGACT CAGAGCGATT ACTGGAACCT TCAATTCCTT GGCTAGTATT TTCAACTGAC 240

GAGAAATTTC AGAAACTTCT TGTTGACGAT TTTCTCGACC AGTTCCCGTG ATAAGTTGCA 300

AATAGTCTAT CAAAATCAAA CCAAGATTTC CAGTTTCTTG AGCCAATTTA CGAGAACGAG 360

AACGAATCTC TGTAATCCGA ATACCTGGCG TATCATCGAT ATAGATACTG GCGTTAGcTA 420

GATTACCCTG AGCAATAGTA TATTTTTGCC ACTCCTCATC TGTCAATTGC CCTGTACGGA 480

TAGAATGTGA CTCCACTAAG CCTTCTGCAG CTAACATACG ATCTACCAAG CTTTCCGCAC 540

CCATTTCGAG TGAAAAAATA GCAACCGTTT TGTCCAACTT AGTCCCAATG TTCTGAGCGA 600

TATTCAAGGC AAATGCTGTC TTACCAACTG CTGGACGAGC TGCTAAGATA ATCAACTCCT 660

CCTCATGAAG TCCTGTTGTC ATATGATCCA AATCACGATA ACCTGTCGCA ATACCTGTAA 720

TATCGGTCGT TTGTTGCGAG CGAGCTTCCA GATTTCCAAA GTTGAGATTC AACACATCTC 780

GAATGTTCTT AAACCCGCTT CGATTTGCAT TTTCACTGAC ATCAATCAAC CCTTTTTCTG 840

CCTGAGCAAT AATTTCATCA GCTGGTTGTG ACGCTTCGTA AGCTTGGTTG ACAGACTCTG 900

TCAACTTGGC AATTAAACGA CGTAGCATTG CTTTTTCTGC AACAATCTTA GCATAATACT 960

CCGCATTAGC AGAAGTTGGC ACAGAATTAA CAATCTCAAC CAAGTAAGAC AAGCCACCAA 1020

TATTCTGTAA ATCACCTTGA TTATCAAGGA TAGTACGAAC CGTTGTTGCA TCTATGGCAT 1080

CACCACGATC GGATAAATCG ACCATGGCTT GGAAAATCAA ACGATGGGCA TACTTAAAAA 1140

AGTCCCGAGA CTCAATGTAT TCTCGCACAA AAACAAGTTT ACTCTCATCA ATAAAGATAG 1200

CCCCTAAAAC GGATTGCTCA GCTAAGATAT CTTGAGGTTG TACTCGTAAC TCTTCTACTT 1260

CTGCCATCAG ACTTCCCTTC CTTTTACAAT CTTGTCAAGA AGGTGTAAAC TTATCCTTCT 1320

TTCACACGAA GATTGATTAC ACTTGTGATA TCTTGATAGA TTTTCACTGG CACATCAATC 1380

AAACCAACCG CTCGAATCGG AGCTTGTACT TGAATATGAC GTTTATCAAT CTTAATTCCA 1440

AATTGCTTTT GCAATTCTTC TGCAATCTTC TTATTGGTAA TAGAACCAAA GGTACGACCA 1500

TCTGGACCAA CTTTTTCAAC AAATTCTACA ACAGTTTCTT CTGCTTCAAG TTGTGCTTTA 1560

ATTGCTTTTC CTTCTGCAAT CATCTCAGCG TGAGCTTTTT CTTCCGATTT TTGTTTACCA 1620

CGAAGTTCAC CTACAGCTTG AGCAGTCGCT TCTTTGGCTA GATTCTTTTT GATAAGAAAG 1680

TTTTGCGCAT ACCCTGTTGG TACTTCCTTA ATTTCGCCTT TTTTACCTTT TCCTTTAACA 1740

TCTGCTAAAA AGATTACTTT CATTCTTCTT TCTCCTTTTC CTTCATTTCA TTTAATACAA 1800

TTTCTGTCAG TTTTTCACCT GCTTCTGACA AGGTTACATC TTTAATTTGA GCTGCTGCCA 1860

AATTAAAGTG GCCTCCACCG CCTAACTCTT CCATAATCCG TTGTACATTC AGTTTACTAC 1920

GACTTCGAGC TGAGATAGAG ATAAATCCTT GTGTATTCTT CGCAAGAACA AAACTCGCTT 1980

CAATACCTGA CATGGCTAAC ATGGCATCTG CTGCCTTACT AATAACAACT GTATCATAGC 2040

ATTTCATGTC CTTAGCCTCT GCTATTAGTA CATCTGAACC TAATTTACGC CCCTGTAAAA 2100

TAAGTTCATT GACCTCACGA TATTCTTCAA AATCTGTCGC AGCGATTTCC TGGATAGCAA 2160

TACTATCACT TCCGCGCGTT CTGAGATAGC TAGCAACATC AAATGTCCGA CTAGTTACTC 2220

GCGAGGTGAA ATTTTTAGTA TCCAACATCA TACCAGCCAT CAAGACACTT GCTTGCATAC 2280

GACTCAAACG ATTTTTCTTA GAATTCTGGA ACTGAATCAA TTCCGTTACC AACTCACTGG 2340

CACTACTTGC ACCACTTTCG ATATAAGTAA TAACCGCATT ATCTGGAAAA TCCTGATCCC 2400

TTCTATGGTG GTCAATAACA ATGGTTTGGG TAAATAAATC ATAAAATTCT TTTGATAATG 2460

TTAAGGCTGT CTTTGAATGG TCTACAAGAA TCAACAAAGA ACGATTGGTC ACCATCCCCA 2520

TTGCATCCTT AACAGACAAC AACTTCGTAA CTCCTTCTTT TTCTATGAAT GAAACAGCTC 2580

GTTCAATATC TGGAGACATT TGTTCTTCAT CATAAAGAGC ATAGCTATTT TCAATCACAT 2640

TGCTGGCGAA CAACTGCATA CCTACAGCAG AGCCCAAAGC ATCCATGTCT AAATTTTTGT 2700

GACCGACTAC AAAAACCTGA TCTACACTCC GAATCTTATC TGAAATAGCT GTCATCATAG 2760

CGCGCGTACG AGTCCGTGTA CGCTTGATTG AAGCAGCAGA CCCACCACCA AAATAAACTG 2820

GATTTTTCGT TTCGTCGTTT TCCTTAACAA CCACCTGGTC GCCACCACGT ACTTCAGCCA 2880
AGTTCAAATT GAGCAAAGCA ACTTTCCCTA TCTCATCATG ATTTCCATCG CCATAAGAAA 2940
ATCCCATACT TAAGGTCAAG GGCAACTGTC TCTGTTTCGA CTCTTCTCTG AAAGCATCAA 3000
TAACAGAAAA TTTATCATTC ATCAAGCCCT CAAGCACCGT GTAGTCAGTA AATAGATAAA 3060
ATCGATCCAT ACTTACCCGA CGAGAAAACA TCATGTGTTT TTCTGAAAAC TCTGATATAA 3120
AATTAGCTAC AAAACTATTG ATTTGACTAA TATCTGACTC AGAAGTTTCA TCCTCCAAAT 3180
CATCATAATT ATCCACAGAG ACAATCCCAA TCACTGGTCT ACTTGTTACC AATTCATCTG 3240
TTATGGCTTG TTCCCTGGAT ACATCTACAA AATACAAAAC ACCGGAAGAA GCATCCATAT 3300
GAACAGCATA ACGCTTCTCA CCAAGCTTGG CATAAGTAGA CGGATTTCCT ACTGAAGCCT 3360
TGATAATCGT TTGAACAGCT TCTAAATCAA AATCACCATC TTCCTTGGTC AAAATCAATT 3420
CAGCATAGGG ATTAAACCAC TCAACCTCTC CAGAAGATAA ATTCAATTTC ATAACACCTA 3480
CAGGCATCTG TTCCAATAGA GCTGTCAAAC TTTCTTCCGC TTGGTGGTTT ACATACTGTA 3540
TCTGTTCTAC ATCACTCCTT GTATAATGCA CTCTCAGTTT CTTAAATAAA AAAACATAGC 3600
CTCCTACAAA AAGAAACAAA ATTAAAACCG TCAACAGATT ATTATTAACA AAAATAATGA 3660
AAGTGGATAA GACTCCAAAC GCAATCAATC CTACTAGAAT AGGAAAAATT GGACTTACAT 3720
AAAATTTTTT CATTCAAAAC CTCTTGGCAC CCATTATACC ATAATACCCC TCAAAAAGCG 3780
ACTTTTTAAA AGTGTAATCA GTAATTCTAT CAATTATAAG AAAAAGGTAG TTTACAATTC 3840
AGTAAACCTA CCTTTACACA TATTGAAATT AAGATTCTTT AACCTCTAAC AAACCAATTT 3900
CGCCATCCTC ACGACGATAA ATCACATTGG TTGTCTGATC TTCAACATCC ACATAGATAA 3960
AGAAATCATG CCCCAATAAA TCCATTTGTA GAATTGCTTC TTCCAAATCC ATTGGTTTTA 4020
AATCAATTTG TTTTGAACGA ACAACTTTAG ACTGGACAAT ATTTGAATCT TCCACCAAAG 4080
CATCTGTAAA TAATTGACCA GTTGCTACCT TATTTTTATT TTTACGCTCG ATTTTTGTTT 4140
TATTTTTACG AATCTGACGT TCAATTTTAT CAGTTACAAG GTCAATTGAA CCATACATAT 4200
CTTGAGATAC ATCTTCTGCG CGGAGAGTAA TAGATCCAAG CGGAATCGTT ACTTCCACTT 4260
TAGCCGTTTT TTCACGATAA ACTTTTAAGT TAATTCGGGC ATCCAACTCT TGTTCTGGTT 4320
GGAAGTACTT TTCGATCTTT TCGAGTTTAG AAACTACATA ATCACGAATT GCTTCTGTTA 4380
CTTCTAGGTT TTCACCACGG ATACTATATT TAATCATATG AGTACCTTCT TTCTAAACAT 4440
TTTTGTTTTT ATGATTTTAT TATAACGCTT TCATTCTATT TTTGCAAATT TTTTCCTCAT 4500
CTTACAAGGG AAAATGTTTT TACATCCTTA GCACCAGCTT CTTCCAACAG TTTCTTAACA 4560

CGATTTATAG TTGCTCCTGT AGTATAGATA TCATCTATAA GTAGGATTTT TTTAGGAATA 4620

GTGACTCCAC TTTTAATAAA GAAAGGAAGT TCTGTCCCCA AGCGCTCTGA ACGATTTTTA 4680

GAAGAACTGG CTCTCTCTTC TCTTTTCTCT AATAAATCCA GATACTCAAA GCCTGCTGCC 4740

TCTACCAAGC CCTCAACCTG ATTAAATCCT CTATTAGCAT ATCTATCAGG ACTTAGGGGA 4800

ATTACAACAA ATTGATACTC TTTGTACTTT TTCAACTCCT CACTTAAAAA TGAAGCGAAA 4860

ACTTTTCTTA ACAGGAAGTC TCCATCAAAC TTATACCGAC TGAAAAAATC CTTCATAGCT 4920

TGATTGTAAG TAAAAATCGC TCTATGACTG ACTTCAACTC CCTCTTTACA CCAAAGTTGA 4980

CAATCTTGAC ACTTTGTTGA CAACTCTGTT TTCATACAAT TTGGACAGTT CTCTTCCCCA 5040

ATTCTTTCAA AAGTAGAATC ACAGTCTGAA CAAAGACAAG AGTCATCATT CCTCAGAAGT 5100

AAGAGACTAC TAAAAGTTAA AACAGTCTTC ATAGTCTGCC CACATAACAA GCACTTCATA 5160

GACCAGCCTC CTTATTCATC ATCTGAATTT CCTTAATCGC CTTCTTGATT GAAGCATTTA 5220

ACCCATCATG GAAGAAAAGC AAATCTCCTG TCGGTCTATC CATGCTTCGT CCAACTCGTC 5280

CACCAATCTG AATCAAACTA GACTTGGTAA ACAAACGATG ATTGGCCTCT ACTACGAAAA 5340

CATCCACACA AGGGAAGGTA ACTCCGCGCT CCAAGATTGT CGTACTGATA AGTATTGTCA 5400

GTTCTCCATC TCGAAAAGCT TGTACTTGCT CTAATCGATC CTCTGTTACA GAAGATACAA 5460

AGCCAATTTT CTCATTTGGA AATTGCTCCT GTAAGATTTC TGCTAACTGC TCCCCTTTCT 5520

TAATTTCTGA AGCAAAAATG AGTAACGGAT AAGCTGTCTT TCTCTGCTTC TCAATATAGG 5580

ACTTTAACTT TGGTGACAAA CGATTCTTGT CTAAGTAGCG ATTAAAATCC GATAACCAAA 5640

TTGGTTTTGG AATAATCAAC GGATTTCCAT GAAACCGTCT CGGTAAATTC AGTCTTTTTA 5700

GTTCTCCTAA ACGGACCTTT TTATCTAACT CATTGGTCGA AGTCGCTGTT AAAAAGATTC 5760

TCAATCCATT CTCCTTTACA CTATTCTTGA CAGCGTGGTA AAGCATGGGA TTATCAACAT 5820

AAGGAAAAGC ATCTACTTCA TCCACTATCA GCAAATCAAA AGCTTGATAA AACTTCAATA 5880

ACTGATGGGT TGTTGCAACA ACTAGTGGTG TTCGAAAATA AGGTTCCGAT TCTCCATGTA 5940

GCAAAGCTAT CCCGCAAGAA AAATCCTGTT GCAGGCGCTT GTACAGCTCC AAACAAACAT 6000

CTATGCGAGG ACTAGCCAAA CACACTGCAC CACCCGCATT GATCACTTTA GCCACTACTT 6060

GATAAATCAT TTCTGTCTTT CCAGCTCCTG TTACCGCATG AACTAAGGTT GGCTTTTGCT 6120

TGTCTACTAC TTGAAGCAAT CCCTCTGACA CCTTCTCTTG AAAAGGAGTT AATTGGCCGC 6180

GCCATTTGAG AACATCTTGC TTTGGAAAAT CCTCCTGCGG AAAATAGTAT AAAGTTTGAT 6240

CACTTCTGAC TCGCTTCATC AGCAAGCACT CTCGACAATA GTAAGCACCG ATGGGCAAAT 6300

ACCATTCTTC TAGAATAGTA CTATTACAGC GTTGACAGAA AAGTTTCCCC TTCTCCTTTC 6360

TCATTGCTGG AAGTTTCTCC GCCAACTGAC GTTCTTCTTC TGTTAATTCA TTCTCAGTAA 6420

ATAAACGACC GAGATAATCT AAATTTACTT TCATACTTCT TTATTCGTAA AAACTAGCAC 6480

TTTAGATGAT TTTTTAGTAC AATTAAATCA TGGAATTTAG GACAATTAAA GAGGACGGTC 6540

AAGTCCAAGA AGAAATCAAA AAATCTCGCT TTATCTGCCA TGCCAAGCGT GTTTATAGCG 6600

AAGAAGAGGC TCGTGACTTC ATTACTGCCA TCAAAAAAGA ACACTACAAA GCGACACATA 6660

ACTGCTCTGC CTTCATTATT GGAGAACGTA GTGAAATTAA ACGTACAAGT GATGATGGTG 6720

AGCCTAGTGG TACTGCTGGT GTTCCCATGC TTGGGGTACT AGAAAATCAC AATCTCACCA 6780

ATGTCTGTGT GGTCGTGACA CGCTACTTTG GTGGTATTAA ACTAGGCGCT GGAGGACTAA 6840

TTCGTGCTTA CGCCGGCAGT GTCGCCTTAG CTGTCAAAGA AATTGGTATT ATTGAAATAA 6900

AAGAACAGGC TGGCATTGCT ATTCAAATGT CTTATGCTCA GTACCAAGAG TACAGTAACT 6960

TCCTTAAAGA ACATGGTCTC ATGGAGCTGG ATACAAACTT TACAGATCAA GTCGATACGA 7020

TGATTTATGT TGATAAAGAA GAAAAAGAAA CTATTAAAGC TGCACTTGTG GAGTTTTTTA 7080

ATGGAAAAGT CACTTTAACT GACCAAGGTT TACGAGAGGT TGAAGTTCCT GTAAACTTAG 7140

TGTAAACAAT GAATAATACA GCGTTTCGTT GACATTCTCA CAACTACTTT AGCGAGCAAA 7200

ATAAAAAGAG GCGTACCAAA ATATACTAGA AAATGAAGCA ATTCAAACGA AACCTGATAT 7260

CGTTTTCCTT CACACCTATT TACTAGAATT AGCTGAACGC AATCACTTGA AAATTAATGA 7320

CTTTGATCTA TGATATATAG AAATGGTATG GATAGCGTTA TACTAAAGAT ATCTTATACA 7380

AAGAGGTATT CATATGTCTA TTTATAACAA CATTACTGAA TTAATCGGTC AAACACCGAT 7440

TGTTAAACTT AACAACATCG TGCCAGAAGG TGCTGCAGAC GTCTATATAA AGCTTGAAGC 7500

ATTTAATCCT GGTTCATCTG TAAAAGACCG TATTGCCCTT AGCATGATTG AAAAAGCTGA 7560

ACAAGATGGT ATTCTGAAAC CTGGTTCTAC TATTGTTGAA GCAACAAGTG GAAACACCGG 7620

TATTGGACTT TCATGGGTAG GTGCTGCTAA AGGGTATAAA GTCGTCATCG TTATGCCTGA 7680

AACTATGAGT GTAGAACGAC GTAAAATTAT CCAAGCTTAT GGTGCTGAAC TCGTCCTAAC 7740

TCCTGGTAGC GAGGGAATGA AAGGTGCTAT TGCTAAGGCT CAAGAAATCG CTGCTGAACG 7800

TGATGGTTTC CTTCCTCTTC AATTTGACAA TCCAGCTAAT CCAGAAGTAC ACGAAAGAAC 7860

AACAGGAGCT GAGATACTAG CTGCTTTCGG TAAAGATGGA TTAGATGCCT TTGTTGCTGG 7920

AGTAGGTACT GGTGGAACGA TTTCTGGTGT TTCTCATGCA CTCAAATCAG AAAATTCTAA 7980

CATTCAAGTT TTTGCAGTAG AAGCAGATGA ATCTGCTATT CTATCTGGTG AAAAACCTGG 8040

TCCTCACAAA ATTCAAGGTA TCTCAGCTGG ATTTATTCCT GATACACTTG ATACTAAAGC 8100

CTATGATGGT ATCGTTCGTG TAACATCAGA TGACGCTCTT GCACTCGGAC GTGAAATTGG 8160

TGGAAAAGAA GGCTTCCTTG TAGGGATTTC CTCAGCTGCA GCTATCTACG GAGCCATCGA 8220

GGTTGCCAAA AAATTAGGTA CAGGTAAAAA AGTCCTTGCC CTAGCACCAG ATAACGGTGA 8280

ACGTTATCTC TCTACAGCAC TTTATGAATT GTAACCGTCC AATAACGAAG TCTATTGAAA 8340

AATCTCCAGA CTAGAGAACT CACGGATAGT TCCTAATCTG GAGATTTCTT ATTTGCACTT 8400

TTCTTGTACA ACTTTAGTCC ATGGTAAATA GGCCTCTAAA ACCTCTTTGT TTACGAGAGT 8460

TTCCACGTTT GGAAGACATT CTAGAAGATA GGATAGATAT TTCTCACTAT TTATAATGGA 8520

TTGAAATAAG ATATGAACAA ATCGATTAGA ACATGATGGT AAAGCGTAAT CCCTTGTTTC 8580

TCAGCTTTCC CAGACAAAAA AGTCCAATAG TAAGTCAGCT GACTATCACT CTCTAGCACC 8640

CTATAAGAAG TTTCATCCGC ATGAAGTAAG GGCTGAGTCA ATAGTCTCTC TCGCAAGAGG 8700

TTATAAAGGG GCTCCAAATA GTATTGACTC GTCTTGATAT GCCAATTAGA GATTTCCTTA 8760

CGTGTGATTG GTAAACCCAT CCTAGCCCAA TCTTCTTCTT GGCGATAATT GGGTACCTTC 8820

AGATTAAACT TCTGATGGAT GGTGTGAGCG ATAATAGAAG CTGAGCCAAA GTTATGCGCT 8880

AAAGGGGCTT TAGGAATAGG AGCTTTCACA AGCTTATCCA GATGATTATC TTTTACTCGT 8940

TATGGACAAT GCTATATGGC ATAAATCAAG TACCTTAAAG ATTCCGACTA ATATTGGCTT 9000

TGCATTTATT CCTCCATACA CACCAGAGAT GAACCCCATT GAACAAGTGT GGAAAGAGAT 9060

TCGTAAACGT GGATTTAAGA ATAAAGCCTT TCGAACTTTG GAAGATGTCA TACAAGGACT 9120

GGAGAAGGAG GTGATAAAGT CCATCGTTAA TCGGAGACGG ACTAGAATGC TTTTTGAAAA 9180

CAGATGAGTA TAAAAAGAAA GTCCTCATTT CAATAGAAAT CACGACTTTC TGATGAATTT 9240

ATAGTAAAAT GAAATAAGAA CAGGATAGTC AAATCGATTT CTAACAATGT TTTAGAAGCA 9300

GAGGTGTACT ATTCTAGTTT AAATCCACTA TATTTGGGGA GTGATAGAAA AGCCCTTCAT 9360

CAGCCAATCT ACTTGTTCAG GTGCGAGAGC TTTGACATCC TTTTCTGTAC TGGACCAAGT 9420

CAGTTTTCCG TTCTCAAAGC GTTTATATAA TATCCAAAAT CCTTGACCAT CCCAGTAAAG 9480

AACTTTAAAG CGGTCTTTAC GTCCACCACA AAAGAGAAAG ACTTGATCGG AGAAAGGATC 9540

CAATTCAAAG TGGGTTTTAA CTACATAGGC TAATGAGTCT ATTCCCTGCC TCATATCTGT 9600

CTTGCCACAA ACAAGGTGAA CTTGACCTAA ATCACTTAGT TGAATTATCA TAGTACAATA 9660

CCTTTCCTCC GATAATTATT TTTTATCTGG TATACTGGAA GTTGGGGAAT TAGGATAGAT 9720

ACCTTGTTAT GACGCGCTTA CTATGAATTT GAAGTATAGT CTCCTAAATG CACTTAGCCC 9780

TTATTATAGG GCTTTTTGTT TTAATTATTC TAATCGAGTG AGACTGGGGA AAAAACAATT 9840

TCAGGAAAAA TCTAAGCCCT ATACAAAAAA GGAAGCAATT TGCTTCCTTT CTATTATTAG 9900

TTATTCAAGG CTGCTGCCAT TGTAGCTGCA ACTTCAGCTT CGAAGTCGTT TGCAGCTTTC 9960

TCGATACCTT CACCAACTTC AAAGCGAGCA AACTCAACTA CCGAAGCGTT AACTGATTCA 10020

AGGTATGCTT CAACTGTCTT GCTGTCATCC ATGATGTAAA CTTGTGCAAG AAGTGTGTAA 10080

GCTTGGTCAA CTTTAGTGTT ATCAAGCATG AAGCGATCCA TTTTACCTGG AATAATTTTG 10140

TCCCAGATTT TTTCTGGTTT GCCTTCTGCA GCCAATTCAG CTTTGATGTC AGCTTCAGCT 10200

TGAGCAATAA CATCATCAGT TAATTGAGCT TTTGATCCAT ACTTCAAGTG TGGAAGAGCT 10260

GGTTTATTAA CCATTGCACG GCTTTCGTTG TCTTGGTCGA TAACGTGATT CAATTGTGCC 10320

AACTCATCTT TAACGAATTG CTCATCCAAT TCTTTGTAAG AAAGAACTGT TGGTTTCATC 10380

GCTGCGATGT GCATTGACAA TTGTTTAGCA AGTGCTTCGT CTCCACCTTC AACAACTGAA 10440

ATAACACCGA TACGTCCACC GTTATGTTGG TATGCTCCAA AGTGTTGTGC GTCTGTTTTT 10500

TCAATCAATG CAAAGCGACG GAATGAGATT TTCTCTCCGA TAGTTGCTGT TGCAGATACG 10560

TATGCAGCTT CAAGAGTTTC ACCTGAAGGC ATTATCAAAG CAAGAGCTTC TTCGTTGTTA 10620

GCAGGTTTTC CTTCAGCAAT GACTTTAGCT GTAGTATTTA CCAATTCAAC GAATTGAGCG 10680

TTTTTTGCAA CGAAGTCAGT TTCAGCGTTT ACTTCAATAA CTGCTGCAAC ATTACCGTTA 10740

ACATAAACAC CAGTCAAACC TTCTGCAGCA ACACGGTCAG CTTTCTTAGC TGCCTTAGCC 10800

ATACCTTTTT CACGAAGCAA TTCAATCGCT TTTTCGATGT CACCGTCTGT TTCTACAAGC 10860

GCTTTTTTAG CGTCCATAAC ACCGGCACCA GATTTTTCAC GCAACTCTTT TACAAGTTTA 10920

GCTGTAATTT CTGCCATTTT AATTCTCCTA TATTTTTTGA AAATAGGAGA GCGCGGCTAA 10980

GCCCCGCCTC CGG 10993

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8411 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CGACGGGGAG GTTTGGCACC TCGATGTCGG CTCGTCGCAT CCTGGGGCTG TAGTCGGTCC 60

CAAGGGTTGG GCTGTTCGCC CATTAAAGCG GCACGCGAGC TGGGTTCAGA ACGTCGTGAG 120

ACAGTTCGGT CCCTATCCGT CGCGGGCGTA GGAAATTTGA GAGGATCTGC TCCTAGTACG 180

AGAGGACCAG AGTGGACTTA CCGCTGGTGT ACCAGTTGTC TTGCCAAAGG CATCGCTGGG 240

```
TAGCTATGTA GGGAAGGGAT AAACGCTGAA AGCATCTAAG TGTGAAACCC ACCTCAAGAT    300
GAGATTTCCC ATGATTATAT ATCAGTAAGA GCCCTGAGAG ATGATCAGGT AGATAGGTTA    360
GAAGTGGAAG TGTGGCGACA CATGTAGCGG ACTAATACTA ATAGCTCGAG GACTTATCCA    420
AAGTAACTGA GAATATGAAA GCGAACGGTT TTCTTAAATT GAATAGATAT TCAATTTTGA    480
GTAGGTATTA CTCAGAGTTA AGTGACGATA GCCTAGGAGA TACACCTGTA CCCATGCCGA    540
ACACAGAAGT TAAGCCCTAG AACGCCGGAA GTAGTTGGGG GTTGCCCCCT GTGAGATAGG    600
GAAGTCGCTT AGCTTTAATC CGCCATAGCT CAGTTGGTAG TAGCGCATGA CTGTTAATCA    660
TGATGTCGTA GGTTCGAGTC CTACTGGCGG AGTAATtGAT AAAAGGGaAC ACAGCTGTGT    720
TCCTCTTTTT GTATCAATTT GTATCACCAA GCATTTTCAT AAGGAAGTCT GTTATTTCTT    780
GAGAACTTTC TTTTTTTCCA TGTGCAATCC AAGTTTGGCA GACACCAAAA AGTGCATGAG    840
TTAGATAGAT GCTACTATAT TCTAATTCAG TGGTATTTAG ATTCAGTTGC ATAAATCGCT    900
TTTGTAAATC TGTACTAAGC ATGATATGAA GTTTATTTCG TAAGAAATTT TGGATTTCTT    960
TAGTCCCATT TTCAGAAAGA AGGGCAGCCA GAAGTGGTTC TGACTCTAGA TATTCAAAAA   1020
CTTCTAAAAT AGCGTCTCTT TTGTGATGAG CATGTTTTTG AAAAATATAT TCAAATGTAT   1080
GGAATAGCTT GCTTTGATAG TGCTCAATCA TATCATACTT ATCCTTATAG TGAGTATAGA   1140
AGCTGGAACG ACTAATTCCG GCTTTTTCTA CTAATTTGAC AGTAGAAATT TTATCAAATG   1200
GCTGTTCCAT CAGTAATTGT ACCATAGCAT TTTCAATAGT TCGCTTTGTT TTTAAGCGTT   1260
TGTTACTTTC TTGCATATTT CCTCCTTGTA AACAAATTAG ACTATATGTC TAAAAATAGA   1320
TTTTTTATCT TGTAATTTAG ATTTTTTAAT GTATAATCTA TTATATCAAA ATTTTAGACA   1380
ATATGTTTAA AAAAGGAGAA ACTAAGTTTA AAGAATGGAA AGCAATTTAA AAAAAACCAA   1440
CCTTTATTAT TGTCATGATC GGGATTTCTC TTATTCCAGA TCTGTACAAT ATCATATTTT   1500
TGTCATCAAT GTGGGATCCA TATGGGCAAT TGTCTGACTT ACCTGTGGCA GTTGTAAATA   1560
ATGATAAAGA GGCTTCCTAT AATGGTAATA CTATGGCAAT AGGAAAAGAC ATGGTGTCCA   1620
ATTTAAAAGA AAATAAAACC TTGGATTTTC ATTTTGTAGA TGAAGAGGAA GGAAAGAAGG   1680
GATTGGAAGA TGGCGATTAC TATATGGTAG TGACTTTACC AAGTGATTTA TCTGAAAAAA   1740
CAACTACATT ATCCAATATT CAATCGACAG CAGCTTATCA ATCATTGACA AGTGAGCAAC   1800
AAACTGAGAT AAGTGATTCT GTATCTCAAA ATTCAACTGA TAGTATTCAA TCGGCTCAGT   1860
CAATTGTAGC TTTAGTACAA GATTTACAGG GAAGTTTAGA AAACTTACAA AATCAATCTT   1920
CTAATCTTTC GACTTTAAAA AATCAATCTA ATCAAGTATC ACCTATTACT TCTACTTCTT   1980
TGATAGGATT GTCAAGTGGA TTAACAGAGA TACAAGGAGA TGTTACTAGC AAATTAGTTC   2040
```

CTGCCAGTCA GTCGATTGCA TCAGGTGTAA ACGCATATAC TACAGGTGTT GATAAAGTTT 2100
CTCAGGGCGC AAGTCAACTA AGTGAAAAAA ATGCCACCTT GACAGGTAGT TTGGATAAAC 2160
TAGTTTCAGG CTCAAACACC TTGACACAAA AATCTTCTAG ATTGACAGCA GGAGTTGGTT 2220
AATTACAATC AGGATCTGGG CAATTAGCAG ACAAATCCAG TCAGTTACTT TCAGGTGCTT 2280
CTCCATTAGA GAATAGAGCT AATAAATTGG CAGATGGATC TGGGAAACTA GCAGAAGGTG 2340
GAACAAAGTT AACTTCTGGA TTGGAAGATT TACAGACAGG ACTTGCTTCT TTAGGACAAG 2400
GACTAGGTAA TGCTAGTGAT CAACTCAAAT CAGTATCAAC AGAATCTAAA AATGCAGAGA 2460
TTTTGTCAAA TCCACTCAAT CTTTCAAAAA CAGACAATGA TCAAGTTCCT GTAAATGGAA 2520
TCGCAATAGC TCCTTATATG ATATCAGTTG CTCTTTTTTT GCAGCAATAT CAACAAATAT 2580
GATATTTGCG AAATTGCCTT CAGGACGTCA TCCAGAGAGC CGTTGGGCTT GGTTGAAATC 2640
TTGAGCTGAA ATAAATGGTA TTATAGCTGT TTTGGCAGGA ATTTTGGTAT ATGGAGGAGT 2700
TCAGCTTATT GGTTTAACTG CTAATCATGA GATGAGAATA TTTATTCTCA TCATCCTAAC 2760
AAGTTTAGTA TTCATGTCTA TGGTGACCAC TTTAGCAACG TGGAATAGCC GTATAGGAGC 2820
TTTTTTCTCA CTTATTTTGC TTTTACTACA GTTAGCATCA AGTGCAGGTA CTTATCCACT 2880
TGCTTTGACA AATGATTTCT TTAGATCTAT TAATCCCTGG TTACCAATGA GCTATTCAGT 2940
TTCGGGATTA CGACAAACAA TCTCTATCAA CAAGTCATTT TCCTAGCTGT CATACTAGTT 3000
CTATTTACTA GTTTAGGTAT GCTAGCCTAT CAACATAAGA AAATGGAAGA AGATTAAAAA 3060
AATCGACCGA TTAACTGGTC GATTTTTTAT GCCTTAGATG ACTTTCGTCT GTGATTATAG 3120
ATTCCAAATA GTAAGAGAGA AGTAAAGGAA CAGATTGCTC CAGTAATAAA ACCATTGGGA 3180
ATGAAGGAAA GTGTAATAGT TCCTTTCCCC TTGGGAATGT CAACTTTCAT AAATCCAGTT 3240
TGAGCTTGTT TAATTTCTAT TTTCTTACCA TCTTGGTAGG CAGACCAACC TTTGTCATAA 3300
GGAATGGTGA AGAAAATAGA TGTATCTTGT TGGACATCAT ATGTAGCAAA AACCTTGTTT 3360
TTAGAAGTTG ATACTGTGAC AGGTTGTTCT TTAATTTTTT GAATTGCCTC GGTGAAAGTT 3420
TTGGTATCTA AACGATAGAA GGTAGGAGAT TCAAATGATA CTTGTGAATT TCCAGGGAAA 3480
CTAACATTGA TATTGAAAGT TTTTTTCTCT TTAGTATATC CTAGATTAAA GAAGGAGAAG 3540
ACATTATCAG TTGTAAAAGT CTTTTTTTCA CCATTTACAA GGATGTCAAC CTTCTTTTGT 3600
TTATCGTTAG AAAAGTGAAG GTTTATGAAA GAGAGATAAA CTTGGCTGTT TTCTGGAACT 3660
TCAATTTGAT ACTGGATTGC TGCATCTTCA TTTGAAGAAC TTGTGACACT AATCAAATCA 3720
TTAGTATTTT CTATTTTTTC TGTTTTTTCA TAAGGTATTG GAGAAAAATA ATCAAAATTG 3780

ACGTTAGCAA GTTGATTTAA AAATGAGGCC TGATTATCCA AGGTATGTTC ATTGAACTTG 3840

ACATCATTGT AAACAGATTG ACTCGCAACT GCAATCGGAA GAGAGTATTG ATTTTCATAT 3900

AGGGTAAGAT TATCTTTTTG ATAGATATCT TTAAAGCCAT ACTTATCAAT AGGACTGTCT 3960

GAGATATTGT ACTGGATACC AAATAAACTA TCAGCCAAAA TACTATTATT TGCATATCGG 4020

AGATTGAGAT TAGTCCCAGA GGATTTAAAA CCAAGTTTAT CTAAAGTAGA GCTTGATGAA 4080

CGATTTCGAA CAGATGAAAA TTGAGAGATT CCATTGTAGT TGAATTTCAT ACTGTCATTT 4140

CCTGTCTGAG TTTGTAGTTT TTCAGTACGA GTAAATTGAT TTCCAATATA TGTTGAGAAA 4200

GATTCCATAG CTGGGATATC TCGACTATAA GCACTTCGAG AAGCAAATCC CCATTCCTTA 4260

GCAATTCCGT CCATTTGAGA TGAAGCATTT AAACTCATTT CAACCAGTAT AAATAAAGAG 4320

ATTAGAATGG CAAATAGATT CACAGATATA AACTTTTTGA TAACTGCAAG GAGTAAAAGA 4380

GAATAGACAA CCAAAAATTC AAGAGTAAGC AGAATATTCA AATCTGTTAA AAAAGAATAA 4440

TGCGATTTTA GATAGATGGT AGCTAAAAAT CCTGCTACTA CAAGAAAAAG CGAAACTAAA 4500

AAATTCCAGA CTTTAAGTTC TTTCAGACGC TTTAAGACTT CTGCTGCTGT GTAAATTAAC 4560

AAGGTAGAGA AAATCCAAGC ATAGCGATGT AAAAACATGT TTGGAGTATG CATGCCTTGC 4620

CAAAATAAGT CAAGAGCTTC TATGTAAAAG CTTGCAATTA GAAATGCAAA GAATATTACA 4680

TATATGAGTT TCACGTGAAA CTTAATAGAT TTCAGCGTAA AAAATAAAAT GGTCAAAATA 4740

AAGGGAAATA GTCCAACAAA AATCATTGGG ATGGCCCCAT ACTTTGTTGT GTCAAAGGAA 4800

CCAATGAATT GCTTAGCAAA GAGATCAAGA TACCAGCTAC TTTCAGTTTG AAACTTTGTA 4860

ACTTCAGTCA ATTTTTCCCC ATGTGTCTGT AAATCAAATA GAGTGGGAAG AGTCATAATC 4920

AAACTAGCCA TACCAGCTAA AAAGGAGATA ACTATGAAAT CAAGAACAGA TGATTTTCGA 4980

GTCTTAAAGT CCCACGAAAT TTGACAGAGA TACCAGAAAA TAAGAAACAA TACTGTCATA 5040

TATCCAAAAT AATAATTTTG AATAAATAAG ATTGACAGAC TTGTAAAGTA CAATAGGAGT 5100

TTCTTTTCAG TTATCAGTAG ATGTAAACCA GTTATAATTA AAGGAATCAA GATAAAAACA 5160

TCTAGCCAGG TTTTTATCTC TAATTGACTG ACAGTGAAAC TCATCAGAGC ATAGGAAGTA 5220

GATAAGGCTA GTTTTAAAAT CTGAGGGATA GATTGAAACA ATTTATTCAA ACTAAAAAAG 5280

GTTGACAGAC CAATCAATCC AAATTTTAAG AGAGTTGTCA GATAGATAGC ATCTGGCATA 5340

TTCGTTAGAT CAAAAAAGTA AACCAGAGGC GCGAGAAAAC TACCCAAGTA ATAACTAGAT 5400

AGGGCATAGA AGTTTAGCCC TAGACCACTT GTAAAGGTGT AAAACAGATT ACTATTTCCA 5460

TGTAGGATAT TTCGTAAGGC TACATCAAAA ATAACGTATT GATGAAAGCC ATCTCCTAAT 5520

AGAGGAGAGT TGTCGCTATT CCAGTAGATA CTTTGAGATA GATATACTCC AGACATAATC 5580

ACTACAGGAA TGATGAAAGA AATAAAATAG GTTCGATATG TTTTTAAAAA TGATTTCATG 5640
TTACCTCGTA GAATGATAGA AAACTCAGTT GGTTAACCCA ACTGAGTTTT GAAGTTTTAT 5700
TTAGTCTTTC CAAAGTTCTT TAACTTTTGC TTGTACTTCT GCATTTTCTA GGAATTCATC 5760
GTAGGTTTCA TCGATACGGT CAATGACGCC ATTTTTAGAT AAGACAATGA TATGGTTAGC 5820
CAAAGTTTGA ATAAATTCGT GGTCATGGCT GGCAAAGATG ATTGATTCTT TAAAGTTTTT 5880
CAATCCATCA TTCAAGCTTG AGATAGATTC CAAGTCCAAG TGATTTGTTG GATCATCAAG 5940
TACAAGGACA TTTGATTTTA AGAGCATGAG TTTTGAAAGC ATGACACGAA CTTTTTCTCC 6000
CCCTGACAAG ACATTTACAG GTTTGTTAAC TTCATCTCCA GAGAAGAGCA TACGGCCGAG 6060
GAAGCCACGT AGGAAAGTAT TGTCATCTTC TTCTTTACTT GCGAATTGAC GCAACCAGTC 6120
AAGAATTGAT TCTCCTCCTG CAAAATCAGC TGAGTTATCT TTTGGTAGGT AAGATTGACT 6180
AGTTGTAACT CCCCACTTGA CAGTTCCTTC ATAGTCAATA TCTCCCATGA TTGCACGAAT 6240
TAATGCAGTC GTTTGAATAT CATTTTGTCC AATAAGTGCT GTCTTATCAT CTGGACGCAA 6300
GATGAAACTA ATATTATCCA AGATAGTTTC ACCATCAATC TTTACAGTTA AATTTTCTAC 6360
TGTCAAGAGA TCATTACCAA TCTCACGTTC CGCTTTAAAG TTGATAAATG GATATTTACG 6420
ACTAGATGGC ACAATCTCTT CTAGCTCAAT CTTATCAAGC ATTCTCTTAC GTGATGTTGC 6480
CTGCCTTGAC TTAGAAGCAT TGGCAGAGAA ACGAGCAACA AATTCTTGCA ATTGTTTAAT 6540
TTTTTCTTCT GCTTTAGCAT TACGGTCTGC TAGCAATTTA GCAGCAAGCT CAGAAGATTC 6600
CTTCCAGAAG TCGTAGTTTC CGACATAGAG TTTGATTTTT CCAAAGTCAA GGTCGGCCAT 6660
GTGAGTACAA ACTTTGTTTA AGAAGTGACG GTCGTGGGAT ACTACGATAA CTGTGTTATC 6720
AAAGTCAATC AAGAAGTCTT CTAACCAAGT AATCGATTGG ATATCCAAAC CGTTAGTAGG 6780
CTCGTCCAAG AGAAGAACAT CTGGTTTACC AAAAAGTGCT TTGGCGAGGA GAACCTTTAC 6840
TTTTTCACCG TTGGCCAATT CGCTCATGTT TTGGTAGTGT AATTCTTCTG GAATGTTTAG 6900
GTTTTGAAGT AGTTGAGAGG CTTCACTCTC TGCTTCCCAA CCTCCAAGTT CGGCAAACTC 6960
TCCTTCGAGT TCGGCAGCAC GAACCCCGTC CTCGTCTGAG AAATCTTCCT TCATGTAGAT 7020
AGCATCTTTC TCTTTCATGA TGCTATAAAG TTTTTCATTT CCCATGATAA CGACATCAAT 7080
GGCACGTTCA TCTTCGTAGT CAAAGTGATT TTGACGAAGA ACAGAGAGAC GTTCATCTGG 7140
ACCAAGAGAG ATGTGACCAG TAGTAGGTTC GATATCTCCA GCTAAAATTT TTAAAAAGGT 7200
TGATTTTCCG GCACCATTAG CACCGATTAA TCCGTAAGTA TTTCCTTCTG TAAATTTGAT 7260
ATTGACATCA TCAAAAAGTT TGCGATCACT AAAACGTAGT GAAACATCAG ATACTGTAAG 7320

CAATGTTTTT CTCCTATATG TGTAATATAT TTATTCTACT AGAAAATACA GAAATATTCA 7380

AATTTTTATT TGTCAATTTT GTGTAAATTA TATTTACAGT ATCCTTTACA CAAATCTGTA 7440

AAAAGCAAGG CTGATTTATT TTGATAAATT ACGGTTATTT CATTAAAAAA ATGCTATAAT 7500

TGAAAGGACT ATATCGAAGG AGAACAAAAT GACTAAACCC ATTATTTTAA CAGGAGACCG 7560

TCCAACAGGA AAATTGCATA TTGGACATTA TGTTGGAAGT CTCAAAAATC GAGTATTATT 7620

ACAGGAAGAG GATAAGTATG ATATGTTTGT GTTCTTGGCT GACCAACAAG CCTTGACAGA 7680

TCATGCCAAA GATCCTCAAA CCATTGTAGA GTCTATCGGA AATGTGGCTT TGGATTATCT 7740

TGCAGTTGGA TTGGATCCAA ATAAGTCAAC TATTTTTATT CAAAGCCAGA TTCCAGAGTT 7800

GGCTGAGTTG TCTATGTATT ATATGAATCT AGTTTCGTTA GCACGTTTGG AGCGAAATCC 7860

AACAGTCAAG ACAGAGATTT CTCAGAAAGG ATTTGGAGAA AGCATTCCGA CAGGATTCTT 7920

GGTCTATCCA ATCGCTCAAG CAGCTGATAT CACAGCTTTC AAGGCTAATT ATGTTCCTGT 7980

TGGGACAGAT CAGAAACCAA TGATTGAGCA AACTCGTGAA ATTGTTCGTT CTTTTAACAA 8040

TGCATATAAC TGTGATGTCT TGGTAGAGCC GGAAGGTATT TATCCAGAAA ATGAGAGAGC 8100

AGGGCGTTTG CCTGGTTTAG ATGGAAATGC TAAAATGTCT AAATCACTAA ATAATGGTAT 8160

TTATTTAGCT GATGATGCGG ATACTTTGCG TAAAAAAGTA ATGAGTATGT ATACAGATCC 8220

AGATCATATC CGCGTTGAGG ATCCAGGTAA GATTGAGGGA AATATGGTTT TCCATTATCT 8280

AGATGTTTTT GGTCGTCCAG AAGATGCTCA AGAAATTGCT GATATGAAAG AACGTTATCA 8340

ACGAGGTGGT CTTGGTGATG TGAAGACCAA GCGTTATCTA CTTGAAATAT TAGAACGTGA 8400

ACTGGGTCCG G 8411

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9064 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TGCCGTACTC AAGTACAGCC TGCGCTAAGT TTCCTAGTTT GCTCTTTGAT TTTCATTGAG 60

TATTAGTAAC CAAAATCCGA CCACATAGCC AGCCCCTATG AATATAGCCA TTAAAGCTAG 120

CATGGAATTT AGGAAATTAA AAACCACCGC AGATACAAAG GTTAGCACAA AAACATTAAA 180

AGCAATGGTG TCAGAAGCCA AGACTAGAAT ATAGGGTGTC AACCGATCTA AAGTTTTGGA 240

ATCTAGGAAA AATAAGTGTT TATACATGAT GACCTCCTCT ATGGCTGAAA AGCAAGCCTT 300

TTGTTTTTTT ACCCCAAGAC CCTATGTAGA AAAGTGAGCA AAAACGGGAA GGTCGCTACA 360

ATATTATTGA TCACATGCAC CGCATAGGAT GGATAAATGC TCTTGGTATA GCGGGTCAAA 420

CCAGCAAAGA TGATTCCAAC TGTTGCAAAG ACGAAGATAT CTAACAGACT AGGCAGGCTT 480

GAAAAATGAG GGAGAGCAAA TAAAATAGAA GGAAGAAGCA AATCAAGACC AAATCGCGAA 540

TGCTTAAAGA AAGCATGTTG CAGTAATCCT CTATAAATCA ATTCTTCCAT CAGTGGAACC 600

AGAAAGAACA GGGCTATATA AATACCTAGC TCTGCAAAGT TAGTCCCACT ATAACCAATC 660

AATACAGCCC AACCTTCCGC AGTTGACTGA ACATGTTTAG CTGTCTGAAC GTTAAAAGAG 720

ATCTGGAACA CTAGCACTAA TACTGTCAAA ATCGAATACC AAAGCCATTT TTTTCTTGGA 780

ATGCGGAAGA GATAACCATG GCCTGTCTTA ACAAGAACCA CAATCATGAC TCCAATAAAA 840

AGTAAACTCA AGATATTTTG AATCCAGAAT AAATTGCCTA TCTGAGAAGA AAATTGCCAA 900

TAGTTTTGGA CGATAAGCGT CAGCTGAGAA AGACTAAATA CGAAAAATAA GTAAGAGAAG 960

ACTGCACTTA TTTTGAATAG AAGTTGATAC TTTTTCATAG AAATCCTCCC TACTATGACC 1020

TCACCTTGTC AGGCTCTACT GCTGTAAGAT TAAGAAGACA GTTTGTTTTT TTTAAGGCTA 1080

ACCTGACTAC TAGATAATAG ATACATTAAG GCATTAAAGA CAATGAAAAT ATGTCCATAG 1140

AATAAAATCA ACCTCGCATC CAAACCAAGA TAAAGTTTGA TTATCAAAAA GATGAGCAAA 1200

AGAATTTGAA ACCATAAGGT TTTTCCAAAA ATAAATTTAA AGCGATTTCG AATATCTACT 1260

TCCTTGATTT TTACCGCCAC CCCTTTATTA GCAAGAAGGA AAACTCCTGC TTCAAACAAA 1320

CCACTGTAAA GAACAAGCCA CCCAATAGAT ACGATAGAGA TTTGTAAAAA TGTCCCTAAA 1380

AGAATATCCA ACACACTACT CAAGAAAATA ACAAAAAATA ATCTGTATTT CATATTAAAT 1440

ACCTCCATTC ATTTATTTCA CTAACAATTT AATAGAGCCT TCTACTCAAA TATCCTGTCA 1500

GAAAAGGATA GAAAGCTACT TTTTATAATA CTTCAAGCCC CACATGAGCA GAAGCGTGAT 1560

AAACAAGCAG AGAATACACC TATATAAGCG ATTAGTTGTT GATAGAATTC TGTTTCTGAA 1620

ATACCTCTAT ACAAACAAAT GACAAACATA AAATCTGCCA AGCCGATAAA CATAAGTTGA 1680

TTGGTTCTAG GACTAACCAA ATCATCATTT ACTTATATTT AAGAGTATCT CTTTTATTTT 1740

AATGTATGTT AGCACTGAAA AGCAAGACAG GCCAATAATA TTTAAAATGA ACAGTAACGG 1800

GGTTAAGTCT CTAAAAAAAT TATCTACTGA CACTACAAGA AATACTATAC ATATTATAGT 1860

CGAAACTATC TTTTTCTTAT CCATAATTAT TTACTCCTTT CCTAACAAAT CCAGCTTATC 1920

AATCAAGAGC GATTTTTAAC ATAATGTAGC AGCACCCGTT GCAACTTTGA CAAGTTTAGT 1980

ATATCATTGT TTTTTAAAAT TTTTCATCCA AATCTTGAAT TGTCATCGAA ACATCTTGAA 2040

TTGTTAAAAA ATTTAAAAAG TAAGCATTAA AAACATACTT TCCTCTTTAT ATTGTATTGA 2100

TACCAACTTG TTTGTAGACT TTTCATCCTG CTATCACATA TCATTTTGAC AGGCGAAACA 2160

ATATTAAAGA AACTCCCCTG TAAATTAAGC TAGCAAATAC AGGGGAGAAA TTTATTTTTT 2220

AGAGAGTACT ATCCGTATCC TTTTTGGAAG ATTTTGAAAA TATTTTTCTA ATTAAGTCAT 2280

CCATATAAGG ACCAAATATA CCAACTACTA AACCAATAAT AAAACTTTTA AAATCCATAA 2340

TTACCACCAA CATATTGCTG CATAGGCTAC ACCTCCAAGT ATAGCTCCAC CTGCAGCACC 2400

AGTTACACCT ATTCCTATAG CAAATGGTCC CAATAGAAAT GTCAAACCGT TGTTGCACAC 2460

CCATCAATTG CGCCATATGC AACCCCTGCT GCACAACTAA TTTTTCTTCC CCAATCAATA 2520

TCTCCACCTT CAACGCAAGC AAGCATTTCA TTATCCATAA CTGCAAATTG TGACATCATT 2580

TTTGTATCCA TATAGTGTAT CACTTTTCAG TTACGGAACA AGTTTAATAT AAAAATTATC 2640

AAAAAAACAT AGGCAATAAA GAGAAAAATT AATTTATCAT AGATTAGAAA TAATATGACA 2700

AAACAATTCA ATGATGTTAA TTCAATAGTC TTTTGTTTTT TATCGGAGAT ACTTATGGAT 2760

AGATAAATAA GATAGGTTTG AAAAGCGAAG AGAATAATAA AGAATATAGC CTTCATAAAA 2820

TTTAGCTTTC ATTTTTATGA TGTAGCGGTA TAGGCTAAAT ATCCACAAAC CACTGCTCCT 2880

CCAATTCCTC CTATTGCAGC GCCCCATGGT CCTAGAAGTC TCCCATATTT CACTCCACCC 2940

GCTGCACAAC CTAAAGCAGC AACTACAGCT GCTCCTCCGG AATTACCTCC ATAAACCTCA 3000

CTCAGCATTG TTTCATTTAT ATTACAATAA GTATTCATAC AAGTCTCCTT TTATTAAAAT 3060

CCACCCGTTG CCCCTGTTAC TCCTGCCCAA AGATCCACAC CAAATTTAGC TCCTATGTAT 3120

CCACATGCTC CCATAAATGG TGCTCCAACA CCACTCGCAG CACAAATAGC TGTCCCTAGC 3180

CCCCAGCCAC CAAAAGCAGC ACCACCACCT TCTAAGACAT TAGTTTGCCA ATTATTCTTG 3240

CCTCCTTCAA TACTAGATAA CATAGTTATA TCCATTTCAT GAAATTGTTC CATAATTTTT 3300

GTATCCATGA CAAATACTCT TTTTTATTTT TAATTTTTGT CTTGTTGTAA CTTTGACAAG 3360

TTTAGTATAT CATCGTTTTT TAAAATTTTT CATCCAGATT TTGAATAGTC ATCGAAACGT 3420

CTTGAATTGC AAAAATTACA TTAGACTTCC TGCAAAACTA GAATCCTAGT TCATGATTGA 3480

TAATACCAGC ACTCAAATTC ATTCGTAATC CGAAGCGTTT ACGATGACTT CGATAGGTTG 3540

TTGAAAACAT TTTAAACGTT TTTACTTTGG CAAAGATGTT CTCAACCTTG CTTCTCTCCT 3600

TAGATAGCGC ATGGTTACAG GCTTTATCTT CAACTGTTAG CGGTTTGAGT TTGCTGGATT 3660

TACGTGAAGT TTGTGCTTGA GGATATATCT TCATGAGCCC TTGATAACCA CTGTCAGCCA 3720

AGATTTTACC AGCTTGTCCG ATATTTCTGC GACTCATTTT GAACAACTTC ATATCATGAC 3780

AATAGTTCAC AGTGATATCC AAAGAAACAA TTCTCCCTTG ACTTGTGACA ATCGCTTGAG 3840

TCTTCATAGC GTGAAATTTC TTTTTACCAG AATCATTCGC TAATTCTTTT TTTAGGGCGA 3900
TTGATTTTTA CTTCCGTCGC ATCAATCATT ACCGTGTCCT CAGAACTGAG AGGAGTTCTT 3960
GAAATCGTAA CACCACTTTG AACAAGAGTT ACTTCAACCC ATTGGCTCCG ACGGAGTAAG 4020
TTGCTTTCGT GAACACCAAA ATCAGCCGCA ATTTCTTCAT AAGTGCGGTA TTCTCGCACA 4080
TATTGAAGAG TGGCCATAAG AAGGTCTTCT AGGCTTAATT TAGGTTTTCG TCCACCTTTT 4140
GCGTGTTTAA GTTGATAAGC TGTTTTTAAT ACAGCTAGCA TCTCTTCAAA AGTCGTGCGC 4200
TGAACACCAA CAAGACGCTT AAATCGTGCA TCAGTTAGTT GTTTACTTGC TTCATAATTC 4260
ATAGAACTAT AGTAAAATGA AATAAGAACA GGATAAATCG ATCAGGACAG TCAAATCGAT 4320
TTCTAACAAT GTTTTAGAAG TAGAGGCGTA CTATTCTAGT TTCAATCTAC TATACTATAC 4380
CATATTTTGT TTCGCAGGGA ATCTATTATA AAAGGGTAAG TATTGCAAAA ACACTTACCC 4440
TTTTCTTTTA TACTTCATTA AGCTCTACTT TTTATAATAC TTCAAGCCCC ACATGAGCAG 4500
AAGCATGATG ATTAAGCAGA GAACAGCGCC AATATAAGCG ATTATTTGTT GGTAGGATTC 4560
TCCTGCTGTG ATACCTCTAT ACAAACAAAT AATAGACATA AAACCTGTCA AGCCGATGAA 4620
CATAAGTTGA TTGGTTCTAG GACTAACCAA ATCATCATCT TCAAACTCTC TTATCCTCAT 4680
TTCCCTAGTG AGATAAACAG TAACCAAAAT AGAAGCCAAG TTAATAACTA CTAAAAGAAA 4740
TTGGAAAACT ACGGAAAAAT TTAAAAACTG ACGAGATAGA AATAGATAAG TAGAAACAAG 4800
CAAGGGCAAC TGACCTAAGA ACAATCTCGC AAGGAAGATG TTCCGTTTTT TAGCAAGAAA 4860
AGTTTTCATT TCTTTTCTCC TTTCTTTTTA TTGATAGCAA AATAGATCAT AACTGCAATC 4920
ACATAGGCTA TGGTATAAAA TAGCTGATAC CAAGCACTCT CCCTAAGCGG ATATAGAAAG 4980
ATGGACATGA TTAGATACAG AACGAAAATA ATCAGTATTT TTTTCTTCAT AAGATTTCCT 5040
CCTAAATGTG CGATTTATCT TAGTTGAGCA AGAACATTTA CACTGCTAGT ATAGCACTTA 5100
TTTTGACCTT GGATCACTCA AATCATAAAT GGTCATCAAA ACCTCTTGAA TTGTAAAAAT 5160
TAAAAAAGCA AGCATGAAAA ACATACTTTC CTCTTTATAT TGTATTGATA CCAACTTGTT 5220
TGTAGACTTT TCATCCTGCT ATCACATATC ATTTTGACAG GCGAAACAAT ATTAAAGAAA 5280
CTCCCCTGTA AATTAAGCTA GCAAATACAG GGGAGAAATT TATTTTTTAG AGAGTACTAT 5340
CCGTATCCTT TTTGGAAGAT TTTGAAAATA TTTTTCTAAT TAAGTCATCC ATATAAGGAC 5400
CAAATATACC AACTACTAAA CCAATAATAA AACTTTTAAA ATCCATAATT ACCACCAACA 5460
TGTTGCTGCA TAGGCTACAC CTCCAAGTAT AGCTCCACCC GCAGCACCAG TTGCTGCACC 5520
TTGCCATGTT CCTGTTTTAA TGCCTAGTTG AAGACCTCTT GCTGCTCCTC CTCCAACACC 5580

```
TGCTTTGGCA AAATCTCCCC AATTGCATCC GCCACCTTCA ACGCAAGCAA GCATTTCAGT   5640
ATCCATAACA GAAAATTGTG ACATCATTTT TGTATCCATG ACAAATACTC CTTTTTTAAA   5700
AAACTAAAAT AAATCAGAAT AGAATCCTCA TAATTTTACT ATAAGTCTTA CCAACTTAGT   5760
CCCAATTTAT CACCAACCAT ACCTCCTAAG CATGTTAATC CACCCCCAAT TGCACCAATG   5820
TGTGCTCCAA CAAATGCACC AGCAAGTCCA GCTACTCCTA AAGTGGCCAA ACCTGCTCCA   5880
GTTCCACCAG TTATAATTCC CGTAGTGACT CCTGTAATCA GTGCATTTTG ACAATCAGTG   5940
GAGCTATACC CCCCTTCAAC TTTCGCAAGC ATTTCAGTAT CCATAACCTC TAACTGTGAC   6000
AACATTTTTG TATTCATGAT GAATACCTCC TTTTTATTTT CAATTTGTTA CCAAAGTCTT   6060
AAATTCAATA AACAAATAGA TTTTTTATAG TATCTTTTTG ATTTTCTTAA AAAAGTATAT   6120
ACGTCTACTA TCTTCTTAAA GGTAGCAGTA CCTATTTTTT AGTCTAAGAT TTCAATAATC   6180
TTGAGTATCT AAAATATCTT AATTTCGTTA TTCTCCTTGC AATAAAAAGT TTTACTATAC   6240
TATTTATTAA CTTGCAGAAA GCAAAAAATA TTAGTAAATA ATAGTTTATA GTTAAGTTTT   6300
TTATTCCTAC CAATCCATCA ACTAAGTAAA GCATCAACGA TTACATAAAC GATTGATAAT   6360
ATAATTAAAA TTTTGCTAAC TATCTTATTC TCATCATTCT TAGATAACTT TGATATTTTG   6420
TAAGTAAGTA AATAAGACAG TAAATTAATA GCGATAATAA TACTATATTT AAGAATCATA   6480
ATCTTACAAA GAGGACATAA TTCCTGAACC TACACAAATA AGTGTTGCTG CTCCCCCAGT   6540
TATCGGACCA GTCGCAGCAG CTAATAGTAC TGCTCCAATA CAACCACCGA TTGCAGATCC   6600
TAAATTGCCT CTTCCTCCAC TAACTATTTC GAGTTCTTCA TTATCCATAA CAGAAAATTG   6660
TTCCATCATT TTTGTATTCA TGACAAATAC TCCTTTTTTC TTTTTTTATT TTTGTCTTGT   6720
TGTAACTTTG ATAAGTTTAG TATATCATCG TTTTTTAAAA TTTTTCATCC AGATCTTGAA   6780
TTGTCATCGA AACGTCTTGA ATTAGCTTTT TTATTTCAAG CCACCTCTAA ATGTTTAAAA   6840
AAAATAATTT CTAATCACTT TTTTACCATT CAGGAAGTTT TAATGACTAT TCAAGATTTC   6900
ATAAAATATG AACTTAGTTT TATGACATAA TAGACCTATC CACTATATGA AAGGAATTGC   6960
CAATGACTTC TTATAAACGT ACATTTGTTC CTCAAATAGA TGCGAGAGAC TGTGGTGTCG   7020
CTGCCTTAGC CTCGATTGCT AAATTCTATG GTTCAGATTT TTCTCTAGCT CACTTGAGAG   7080
AACTTGCAAA GACCAATAAA GAAGGGACGA CTGCTCTTGG CATTGTAAAA GCCGCTGATG   7140
AAATGGGCTT TGAAACAAGA CCTGTTCAAG CAGATAAAAC GCTCTTTGAC ATGAGTGATG   7200
TCCCCTATCC ATTTATCGTT CACGTTAACA AAGAAGGAAA ACTCCAACAT TACTATGTTG   7260
TCTATCAAAC AAAGAAAGAC TATCTGATTA TTGGTGATCC TGACCCTTCT GTAAAAATCA   7320
CTAAAATGTC AAAAGAACGC TTTTTCTATG AATGGACTGG AGTAGCTATT TTTCTAGCTA   7380
```